

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 534 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAAGCAGTGT GTATCTATGA TTATATCTCT GTTCATCTAT ATATTTTGA CATGTAGCAA 60
 CACCTCTCCA TCTTATCAAG GAACTCAACT CGGTCTGGGT CTCCCCAGTG CCCAGTGGTG 120
 15 GCCTTTGACA GGTAGGAGGA TGCAGTGCTG CAGGCTATTT TGTTTTTTGT TACAAAAGTG 180
 TCTTTTCCCT TTTCCCTCC ACCTGATTCA GCATGATCCC TGTGAGCTGG TTCTCACAAT 240
 20 CTCCTGGGAC TGGGCTGAGG CAGGGGCTTC GCTCTATTCT CCCTAACCAT ACTGCTCTCC 300
 TTTCCCTTG CCACCTAGCA GTTATCCCC CAGCTATGCC TTCTCCCTCC CTCCCTTGCC 360
 CTGGCATATA TTGTGCCTTA TTTATGCTGC AAATATAACA TTAACTATC AAGTGAAAAA 420
 25 AAAAAAAAAA AAAACTCCAA GGGGGGCGG GTACCAATT CCCCTATAN TGAGTCNTAT 480
 TACAATTAC TGGGCCGTCG TTTTACAACG TCGTGAATGG GAAACCTGG GCGT 534

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(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCCACGAGTC CGGATGAGC TCAGCCGGG CCGACCACTG GCGTGGTTG CTGGTGCTCA 60
 45 GCTTCGTGTT TGGATGCAAT GTTCTTAGGA TCCTCCTCCC GTCCTTCTCA TCCTTCATGT 120
 CCAGGGTGCT GCAGAAGGAC GCGGAGCAGG AGTCACAGAT GAGAGCGGAG ATCCAGGACA 180
 TGAAGCAGGA GCTCTCCACA GTCAACATGA TGGACGAGTT TGCCAGATAT GCCAGGCTGG 240
 50 AAAGAAAGAT CAACAAGATG ACGGATAAGC TCAAAACCCA TGTGAAAGCT CGGACAGCTC 300
 AATTAGCCAA GATAAATGG GTGATAAGTG TCGCTTTCTA CGTATTGCAG GCTGCCCTGA 360
 55 TGATCTCACT CATTTGGAAG TATTATTCTG TCCCTGTGGC TGTCGTGCCG AGTAAATGGA 420
 TAACCCCTCT AGACCGCCTG GTAGCCTTTC CTAAGTAGAGT AGCAGGTGGT GTTGAATTA 480
 CCTGTTGGAT TTTAGTCTGT AACAAAGTTG TCGCTATTGT GCTTCATCCG TTCAGCTGAA 540

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CAGGAGGATG GATACAGCCG CGAGGCTAAA AAACGGATTT CCTCTTCCTA GCTTAAAATC 600
 TGATTTACAC TGTTTTGT TTAAAGAAAC AAAAGTGCAT AGTTTAGATT TTTTTTTTTG 660
 5 TTGAATATGT TTGTTCTTGG ACTTTATGAG AGAGTCTTAT AAGAATCACG ATTTTCTACA 720
 CCTGTCATTG AGCCAAGAAA GTCCAGTTTA TGACACGTAT GTAGTAGTGA ACACCGTCCT 780
 10 CGATCTGTAC GAAATGTGAA ATGTTTAGGG ACATCTCCAT GCTGTCACCT GTGATTTGCC 840
 CTCTTATGTA TTTTGGTCAT ATTGCCAACT GGAAAGTCAA AATTTTCTAA CAACTTTAAG 900
 TAAGTTCTTT GAAGACTTAG TGCTGTTTTT AATCCAGTTT AGAAAGTAAC TTAATTTTAA 960
 15 TACCACTACT AAAAATTCGA AAATTTCTTC TTAAATCACA TTCAATATGG TTAAAAGAAC 1020
 AACACTAATT GACATTGCGT GGGCTTTTTT TCCCTTTGTT TAAAATGTCA TTTGTTGAGC 1080
 AAGAGTTGTA TAGTATTATC TACTTACTTG AGGCTGTAA TTTTTCATTA CAGTGTTTTG 1140
 20 TAAATGTATC CACGAGACCA TGATGCATTG TTTTGTGCTC AACTTGTGTT TTGTATTTAA 1200
 AGCATTTTGA ATGAAGTGTA TTTTATAAGC ATTTAATATT TATGCTCTTT AGAATGGAAC 1260
 25 ACAGAAAACA AACCTTATAA GTCTGATTA ATCTGAACCA ATAACCTGTG TGGCCTACAA 1320
 AGTATAATTC TATTAAATGT TCCTTAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1374

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(2) INFORMATION FOR SEQ ID NO: 47:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GAATTCGCA CGAGATTACT TGGACATGAA AGAACTCAGG TTCAAGTTTA TTCATTTACT 60
 AAGTTAGTTA AATCATGTGC CTTCCATGAG CCTTCATTTG GTAACCTGGA AAATGGAAAT 120
 45 AATAACACTA GTCATATATA TTCTACACTG CTACCATATG GACCAAAGGG ATTATAGATT 180
 ACAATCACCA TCATTCCTGC TGACAGGTAT ATAGAAAACA ATTTCAATGA AGAAAAGTCC 240
 50 TTACATTTAT CCTTTTCCTA ATATCTGCAT GGGTAACTA ATAAATATAG TCATTAGAAA 300
 ACCCTTATTA TTATTATTAG TTCAATGTGA GAACTGCTGC AGAAAAATA TGCTTTATAA 360
 TATTTTCTTG AATATACATA ATATTCATAA ATTTTCAAAT CATTGAAAAT TACCTTAAAA 420
 55 TTGGAAAAAA TGTGCATTTT TACTCATATA ACAGTATAAA ATTCCTATGT CAATCTCTTT 480
 TTTTTTTTTT TGTMTGAGT TGGAGTCTCG CTCTGTCGCC CAGGCTGGGC AACAGAGCAG 540
 60 GACCCTGTCT TAATTAAAAA AAAAAAAAAA AAACTCGAGG GGGGCCCGGT ACCCTA 596

5 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 851 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

15 CACATGAAGA CACACAGTGG TGAGAAGCCC TTCGCTGCG CCCGCTGTCC TTATGCCTCT 60
CCTCATCTGG ATAACCTGAA ACGGCACCAG CGCGTCCATA CAGGAGAGAA GCCCTACAAG 120
TGCCCCCTCT GCCCTTATGC CTGTGGCAAT CTGGCCAACC TCAAGCGTCA TGGTCCGATC 180
20 CACTCTGGTG ACAAACCTTT TCGGTGTAGC CTTTGCAACT ACAGCTGCAA CCAGAGCATG 240
AACCTCAAAC GTCACATGCT GCGGCACACA GGGGAGAAGC CTTCCGCTGT GCCACCTGCG 300
25 CCTATACCAC GGGCCACTGG GACAACTACA AGCGCCACCA GAAGGTGCAT GGCCACGGTG 360
GGGCAGGAGG GCCTGGTCTC TCTGCCTCTG AGGGCTGGGC CCCACCTCAT AGCCCACCCT 420
CTGTTTTGAG CTCTCGGGG CCACCAGCCC TGGGGACTGC TGGCAGCCGG GCTGTCCACA 480
30 CAGACTCATC CTGAAGTAGG TCCTTCTTCC CCATGTTTTA TACAGACGGA CCAGAAGCCA 540
CCTTTTTCTC CCCCCTGCG CAGGGGCTCC ACACAGACTA ACGTAGGCAC TATAAGGACC 600
35 AGCCCAACCC CATGGGCGGG GGGGCCATA TGGACCAGGG GACCTTGCCT TGAAGGAGGC 660
ACTTCACGAG CTCAGTGAGA AGGGCCCTGT ATTACCTCC ACTGCCCCCA GGGGCTGTGG 720
ACAAACCGGC TGGGGGACTG CCCAGCCTCC CACCTGTTTA TTAACTTAT TTCAGTGCTT 780
40 TATAATAAAG GAAACACTAA CAAAGCCATG TCTATGCTGA ATTGGCAATG GCAGGCAATT 840
TGGCCTTACC C 851

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(2) INFORMATION FOR SEQ ID NO: 49:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GTGAAATGAA AACAGTCTTT TTATAGCCTT TAGCTTGIGA GTTTGGAAGT TTGGGGGGTC 60
60 TTATGTTTGT TTGCTCTT CTGTTCTTG GAGGAGAGTT GAGGCTTTTC TTAGGTGCAT 120

	ACACAGACCC AGGTGAACAC GCTGACTGTG AACCTGCCCT GTATCCGGAG CTGTGCTGGG	180
5	CACTGAGGGG ATGCAACAAA ATTAGGAGAG GWTCCCTTGCT CCCAACGTCT ACTTCTCCTA	240
	CCTCAACAGG GGTCCAGGGT GCAGTGAAC T CAGTTCTTGG CCCTTGGGTG AGGATTCATG	300
	GATGAATGAA AGCTAGACCT GATGGGGAGG CATTATGACT AAATAGGCCC AGCCTCCTTC	360
10	CCTTCCAGCT CTGTCCTAGG AGCATAGGCG GGAAATCTGA GTAGAGTCTG ACTGCAGTTT	420
	TTGCTTATGA TTTGTAAAAG CCGTCATGGG GTCAATAAGA AAATAGGGGT GATGGAGGGG	480
15	GAGAAGCCCA GGACTGGGAG AATCGCACGT GCGCCAGGGG TTTTCACCAA GGATTTTCAA	540
	GACAAACTGG AGTAAGAATT AAAGCCCAG AGGATTTAAT TATCCTGGTT TGCAAAAGAG	600
	CCTCCCATGC CAGTACCGCC CAGCCTTGA GCGCGGAATG CTCATGGCCC CTGTGGTCTG	660
20	CTTGTCCTTC AGCCCATGCC CAGCAGATAC CTCTCTGACT GGAGACGGGC TCAAAGCTGG	720
	ATTAGAAAGG GGAGMGGCAC TTGTGACTTT GTTTGACTCT GTGACTCACT TCCTCGCTCA	780
25	CACCTTGTTT GAACTACTGG ACTTTCAACT GGCTTTCCCTT AGGTCAGGCA AGCAGACAGC	840
	TCCCCACTGA AGAGGTCTGT ACAGTGACAA CCCGGGCCGG CAGCAAGGAC ACAGATGCAG	900
	CCACAGTAAG GCTCCATCAG GACTGGGTCA GTGATGGCAA CAGGATGGCC AAGGATGGCT	960
30	CTAGAACAYT CTGTCCATGC GTCACCTCCC CCAGTTTTRT TTTTAGCTTT GGCTTCAGGG	1020
	AGTGACAGCC ATCACAATA GCCACATTCT GCTCTACTCT CCAACATACC AGATTSTACA	1080
35	CTGTGTTTAT TTCAATGAGAC GTGAATGTG CAGAGAGTGG GGGGATTCTG GTTGTTAAGG	1140
	AACCTTACACT GGGGAGCTTT ACTCTTCCGT GTCAACAATG TGAATACATG TTCTCCAGAT	1200
	TAGCCACACA TGCAACATC AGTGTCTTTC TAGCTTTTANC CGAGAAAGAA ACCAGTCCCA	1260
40	GGGAATGAAT GGTGGTCTCC CCACTCCCGG CAGCACTTTA GGCAGCCCAT AAGCTATCGG	1320
	AGAATGTGAA CGCTCACCTT GCTCCGTCAC GGTTCGTACC TACCACATAA ACAGGAAGAA	1380
45	GCCAGTGACC GGAACAGCTC TAGGAATAAC AAGTCAGAAT AGAAGTGTCC TTTATATTAC	1440
	CAGAAAATAT GGGCTTGGCC TAAGTCGCTG TCTCCTAACC TGCCGGGGTC ATTCCCCACC	1500
	AAACACCCCA TACTAAGGAG CCATGAGCCA CCTGGACATT CACCTTTTCT TTGACCATCT	1560
50	GGAGTCTGGG GCAACTTAAG GAAGGCNCCA CACAGTGGTG CAGGCACATT TCCAAGCGTA	1620
	GGTGTCCTG GCTTTTGTGG CCAAAGCTAG TGTATGGTC AACACAGGC CAGGGTCTGT	1680
55	GGGGCACTGA CCTTGAAAGT GGCAAAATGG AGGTTTCACA GGCTGTGCGG GAGCAGGACG	1740
	GCTTGCTTCA TCTAACAATC TCAGTTTCTT TTAATAAAAG AAAGAAAGGA AAAGATTTCA	1800
	TAAGCAGGTG TCAGTGGACA GTTTAAGYAC TTAACCATTT CTCTTTCTTC TTATGGATGT	1860
60	GAACTGTGCT GTGGATAAAT CATTTGTATT TCTTGAATGT TCTCTATGAC TAACAGTTAT	1920

TAAGTCGGTT GTGTATATGT GTAACATAATG TAACTGCCTT TTAATAATTTC ATTACAATAA 1980
 AAATGACTTT GCTCTGAAMA AAAAAAAAAA AAAAATCTGA 2020

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(2) INFORMATION FOR SEQ ID NO: 50:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2432 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

ATGAAGGGTC GTTGGTGGGA AAGATGGCGG CGACTCTGGG ACCCCTTGGG TCGTGGCAGC 60
 AGTGGCGGCG ATGTTTGTCTG GCTCGGGATG GGTCCAGGAT GTTACTCCTT CTTCTTTTGT 120
 TGGGGTCTGG GCAGGGGCCA CAGCAAGTCG GGGCGGGTCA AACGTTGAG TACTTGAAAC 180
 GGGAGCACTC GCTGTGCAAG CCCTACCAGG GTGTGGGCAC AGGCAGTTCC TCACTGTGGA 240
 ATCTGATGGG CAATGCCATG GTGATGACCC AGTATATCCG CCTTACCCCA GATATGCAAA 300
 GTAAACAGGG TGCCTTGTGG AACCGGGTGC CATGTTTCCT GAGAGACTGG GAGTTGCAGG 360
 TGCACTTCAA AATCCATGGA CAAGGAAAGA AGAATCTGCA TGGGGATGGC TTGGCAATCT 420
 GGTACACAAG GAATCGGATG CAGCCAGGGC CTGTGTTTGG AAACATGGAC AAATTTGTGG 480
 GGCTGGGAGT ATTTGTAGAC ACCTACCCCA ATGAGGAGAA GCAGCAAGAG CGGGTATTCC 540
 CCTACATCTC AGCCATGGTG AACAACGGCT CCCTCAGCTA TGATCATGAG CGGGATGGGC 600
 GGCTACAGA GCTGGGAGGC TGCACAGCCA TTGTCCGCAA TCTTCATTAC GACACCTTCC 660
 TGGTGATTCT CTACGTCAAG AGGCATTGTA CGATAATGAT GGATATTGAT GGCAAGCATG 720
 AGTGGAGGGA CTGCATTGAA GTGCCCGGAG TCCGCCTGCC CCGCGGCTAC TACTTCGGCA 780
 CCTCTCCAT CACTGGGGAT CTCTCAGATA ATCATGATGT CATTTCTTGG AAGTTGTTTG 840
 AACTGACAGT GGAGAGAACC CCAGAAGAGG AAAAGCTCCA TCGAGATGTG TTCTTGCCCT 900
 CAGTGGACAA TATGAAGCTG CCTGAGATGA CAGCTCCACT GCCGCCCTG AGTGGCCTGG 960
 CCTCTTCCT CATCGTCTTT TTCTCCCTGG TGTTTCTGT ATTTGCCATA GTCATTGGTA 1020
 TCATACTCTA CAACAAATGG CAGGAACAGA GCCGAAAGCG CTTCTACTGA GCCCTCCTGC 1080
 TGCCACCACT TTTGTGACTG TCACCCATGA GGTATGGAAG GAGCAGGCAC TGGCCTGAGC 1140
 ATGCAGCCTG GAGAGTGTTT TTGTCTCTAG CAGCTGGTTG GGGACTATAT TCTGTCACTG 1200
 GAGTTTGA TGCAGGGACC CCGCATTCCT ATGGTTGTGC ATGGGGACAT CTAACCTCTG 1260

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	TCTGGGAAGC CACCCACCCC AGGGCAATGC TGCTGTGATG TGCCTTTCCC TGCAGTCCTT	1320
	CCATGTGGGA GCAGAGGTGT GAAGAGAATT TACGTGGTTG TGATGCCAAA ATCACAGAAC	1380
5	AGAATTTTCAT AGCCCAGGCT GCCGTGTTGT TTGACTCAGA AGGCCCTTCT ACTTCAGTTT	1440
	TGAATCCACA AAGAATTAAA AACTGGTAAC ACCACAGGCT TTCTGACCAT CCATTCGTTG	1500
10	GGTTTTCAT TTGACCCAAC CCTCTGCCTA CCTGAGGAGC TTTCTTTGGA AACCAGGATG	1560
	GAAACTTCTT CCTGCGCTTA CCTTCCTTTC ACTCCATTCA TTGTCTCTC TGTGTGCAAC	1620
	CTGAGCTGGG AAAGGCATTT GGATGCCTCT CTGTTGGGGC CTGGGGCTGC AGAACACACC	1680
15	TGCGTTTCAC TGGCCTTCAT TAGGTGGCCC TAGGGAGATG GCTTTCTGCT TTGGATCACT	1740
	GTTCCCTAGC ATGGGTCTTG GGTCTATTGG CATGTCCATG GCCTTCCCAA TCAAGTCTCT	1800
20	TCAGGCCCTC AGTGAAGTTT GGCTAAAGGT TGGTGTAATA ATCAAGAGAA GCCTGGAAGA	1860
	CATCATGGAT GCCATGGATT AGCTGTGCAA CTGACCAGCT CCAGGTTTGA TCAAACCAAA	1920
	AGCAACATTT GTCATGTGGT CTGACCATGT GGAGATGTTT CTGGACTTGC TAGAGCCTGC	1980
25	TTAGCTGCAT GTTTTGTAGT TACGATTTTT GGAATCCAC TTTGAGTGCT GAAAGTGTA	2040
	GGAAGCTTTC TTCTACACC TTGGGCTTGG ATATTGCCCA GAGAAGAAAT TTGGCTTTTT	2100
30	TTTTCTTAAT GGACAAGAGA CAGTTGCTGT TCTCATGTTT CAAGTCTGAG AGCAACAGAC	2160
	CCTCATCATC TGTGCCTGGA AGAGTTCACT GTCATTGAGC AGCACAGCCT GAGTGCTGGC	2220
	CTCTGTCAAC CCTTATTCCA CTGCCTTATT TGACAAGGGG TTACATGCTG CTCACCTTAC	2280
35	TGCCCTGGGA TTAAATCAGT TACAGGCCAG AGTCTCCTTG GAGGGCCTGG AACTCTGAGT	2340
	CCTCCTATGA ACCTCTGTAG CCTAAATGAA ATTCTTAAAA TCACCGATGG AACCACAAAA	2400
40	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	2432

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

55	GACGCTGGGG GCGGGTGGGG GCGCGGGTA CCGGGCTGGA CGGCCGGCCG GCGCCCCCTC	60
	ATTAGTATGC GGACGAAGCG GCGGGCTGCG CGGAGNGACG TCCCTGCGAG CCGCGGACCG	120
	AGGCAGCGGC GGCACCTGCC GCGCGAGCAA TGCCAAGTGA GTACACCTAT GTRAACTGA	180
60	GAAGTGATTG CTCGAGGCCT TCCCTGCAAT GGTACACCCG AGCTCAAAGC AAGATGAGAA	240

	GGCCCAGCTT GTTATTAAAA GACATCCTCA AATGTACATT GCTTGTGTTT GGAGTGTGGA	300
5	TCCTTTATAT CCTCAAGTTA AATTATACTA CTGAAGAATG TGACATGAAA AAAATGCATT	360
	ATGTGGACCC TGACCATGTA AAGAGAGCTC AGAAATATGC TCAGCAAGTC TTGCAGAAGG	420
	AATGTCGTCC CAAGTTTGCC AAGACATCAA TGGCGCTGTT ATTIGAGCAC AGGTATAGCG	480
10	TGGACTTACT CCTTTTGTG CAGAAGGSCC CCAAGACAG TGAAGCTGAG TCCAAGTACG	540
	ATCCTCCTTT TGGGTTCGG AAGTTCTCCA GTAAAGTCCA GACCTCTTG GAACTCTTGC	600
15	CAGAGCACGA CCTCCCTGAA CACTTGAAAG CCAAGACCTG TCGGCGCTGT GTGGTTATTG	660
	GAAGCGGAGG AATACTGCAC GGATTAGAAC TGGGCCACAC CCTGAACCAG TTCGATGTTG	720
	TGATAAGGTT AAACAGTGCA CCAGTTGAGG GATATTCAGA ACATGTTGGA AATAAACTA	780
20	CTATAAGGAT GACTTATCCA GAGGGCGCAC CACTGTCTGA CCTTGAATAT TATTCCAATG	840
	ACTTATTTGT TGCTGTTTAA TTAAAGAGTG TTGATTTCAA CTGGCTTCAA GCAATGGTAA	900
25	AAAAGGAAAC CCTGCCATTC TGGGTACGAC TCTTCTTTTG GAAGCAGGTG GCAGAAAAAA	960
	TCCCACTGCA GCCAAAACAT TTCAGGATTT TGAATCCAGT TATCATCAA GAGACTGCCT	1020
	TTGRACATCC TTCAGTACTC AGAGCCTCAG TCAAGGTTCT GGGGGCCGAG ATAAGAACGT	1080
30	CCCCACAATC GGTGTCATTG CGTTGTCTTT AGCCACACAT CTGTGCGATG AAGTCAGTTT	1140
	GGCGGGTTTT GGATATGACC TCAATCAACC CAGAACACCT TTGCACTACT TCGACAGTCA	1200
35	ATGCATGGCT GCTATGAACT TTCAGACCAT GCATAATGTG ACAACGGAAA CCAAGTTCCT	1260
	CTTAAAGCTG GTCAAAGAGG GAGTGGTGAA AGATCTCAGT GGAGGCATG ATCGTGAATT	1320
	TTGAACACAG AAAACCTCAG TTGAAATGC AACTCTAACT CTGAGAGCTG TTTTGTACAG	1380
40	CCTTCTTGAT GTATTTCTCC ATCCTGCAGA TACTTTGAAG TGCAGCTCAT GTTTTAACT	1440
	TTTAATTTAA AAACACAAAA AAAATTTTAG CTCTTCCCAC TTTTTTTTTC CTATTTATTT	1500
45	GAGGTCAGTG TTTGTTTTTG CACACCATTT TGTAATGAA ACTTAAGAAT TGAATTGGAA	1560
	AGACTTCTCA AAGAGAAITG TATGTAACGA TGTGTWITG ATTTTAAAGA AAGTAATTTA	1620
	ATTTGTAAAA CTCTGCTCG TTTACACTGC ACATTGAATA CAGGTAAC TAATTGGAAGGA	1680
50	GAGGGGAGGT CACTCTTTTG ATGGTGGCCC TGAACCTCAT TCTGGTTCCC TGCTGCGCTG	1740
	CTTGGTGTGA CCCACGGAGG ATCCACTCCC AGGATGACGT GCTCCGTAGC TCTGCTGCTG	1800
55	ATACTGGGTC TGCGATGCAG CGGCGTGAGG CCTGGGCTGG TTGGAGAAGG TCACAACCCT	1860
	TCTCTGTTGG TCTGCCTTCT GCTGAAAGAC TCGAGAACCA ACCAGGGAAG CTGTCTGGA	1920
	GGTCCCTGGT CGGAGAGGGA CATAGAATCT GTGACCTCTG ACAACTGTGA AGCCACCCCTG	1980
60	GGCTACAGAA ACCACAGTCT TCCCAGCAAT TATTACAATT CTTGAATTCC TTGGGGATT	2040

TTTACTGCCC TTTCAAAGCA CTTAAGTGTT AGATCTAACG TGTTCAGTG TCTGTCTGAG 2100
 GTGACTTAAA AAATCAGAAC AAAACTTCTA TTATCCAGAG TCATGGGAGA GTACACCCTT 2160
 5 TCCAGGAATA ATGTTTGGG AAACACTGAA ATGAAATCTT CCCAGTATTA TAAATTGTGT 2220
 ATTTAAAAA AAGAACTTT TCTGAATGCC TACTGGCGGT GTATACCAGG CAGTGTGCCA 2280
 10 GTTTAAAAAG ATGAAAAAGA ATAAAACTT TTGAGGAAMA AAAAAAAAAA AAAAAGCTCGA 2340

15 (2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

25 AGTAGGGGAG ACTGAGACTG ACCGGTAGCC AGGCAGGCGG ACGACGCACG CCCGGACAGA 60
 CTGAGCAGGC GCCGGAGAAC CACTCACAGG TTCCCCCGGC CTTTCCCTTT GAAANCTAGG 120
 CTTTTCCTTT TCCCGTGGCG CCCGAGAGAG AATGCTGGAC TCTGCCGACT TCAGCGCAAC 180
 30 TAANGATTTT TCAAGCTAGG GGACAAACGA TCAGCCCAAT CCTGAGAAGG GGGGAACCAA 240
 GCACCCCGTC CCCATCCCCC TCCCCTCCCC CGACTAAACT CGGGCGCCAA ACCCAGCCCT 300
 35 TCTCTAACCA CCTACTTCC TCCTCTCCTT TCTAGCATGG TGGCTGTATG GACAGTCTGA 360
 CAGAACAGAG ACTGACATCT CCCAATCTGC CGGCCCCCA CCTGGAACAC TACAGTGTTC 420
 TGCATTGCAC CATGACCCTG GATGTGCAAA CTGTAGTCGT TTTTGCCGTG ATTGTAGTCC 480
 40 TCCTGCTTGT CAATGTCATA CTCATGTTTT TCCTGGGAAC GCGCTGAATG GAGTCCAGNC 540
 ACCTGAGCTG TCGCGAACTC TCGCTTTGAT TTCATCCGA GAGCCACCGA GAAGAAAAAA 600
 45 A 601

50 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

60 CTCGTGCCGA ATTCGGCAGC AGAGATGGTA CTTTAAAGAG GTAATTAGGT TGCTAAGATG 60

5 GATTAACATC TTTCTCTTGA CACTGAGACT GGGTTCTCCT GGAATGGTT AGTTCCCAAG 120
 AGAGTGAGTT GTTATAAAC AATGCTGCCT CTCTATTTT GCGCTTTTGT TTGACACAAA 180
 CTCGGTCCCC TTCTGTTTCT CTACGATGTT TTGATGCRGC ATGAGGCAGT CATGAGAACC 240
 CACCAGATAC AGCTGCCTGA TCCTGAATTT CCCAGCCAAC AGAACCAAGT GCTAAATAAA 300
 10 ACTCTTTTTA ATAAGTTAAA AAAAAAAAAA AAAAAAAAAA AANAAANANA AAAAAAAAAA 359

15 (2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1141 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

25 GGCACGAGCT GCTGAGGCGT GAGAATGGCG TCCCGCGGCC GGCCTCCGGA GCATGGCGGA 60
 CCCCCAGAGC TGTTTATGA CGAGACAGAA GCCCGGAAAT ACGTTCGCAA CTCACGGATG 120
 ATTGATATCC AGACCAGGAT GGCTGGGCGA GCATTGGAGC TTCTTTATCT GCCAGAGAAT 180
 30 AAGCCCTGTT ACCTGCTGGA TATGGGCTGT GGCCTGGGC TGAGTGGAAG TTATCTGTCA 240
 GATGAAGGGC ACTATTGGGT GGGCCTGGAT ATCAGCCCTG CCATGCTGGA TGAGGCTGTG 300
 35 GACCGAGAGA TAGAGGGAGA CCTGCTGCTG GGGGATATGG GCCAGGGCAT CCCATTCAAG 360
 CCAGGCACAT TTGATGGTTG CATCAGCATT TCTGCTGTGC AGTGGCTCTG TAATGCTAAC 420
 AAGAAGTCTG AAAACCCCTG CAAGCGCCTG TACTGCTTTT TTGCTTCTCT TTTTCTGTT 480
 40 CTCGTCCGGG GATCCCGAGC TGTCTGCAG CTGTACCCTG AGAACTCAGA GCAGTTGGAG 540
 CTGATCACAA CCCAGGCCAC AAAGGCAGGC TTCTCCGGTG GCATGGTGGT AGACTACCCT 600
 45 AACAGTGCCA AAGCAAAGAA ATTCTACCTC TGCTTGTTTT CTGGGCCTTC GACCTTTATA 660
 CCAGAGGGGC TGAGTGAAAA TCAGGATGAA GTTGAACCCA GGGAGTCTGT GTTCACCAAT 720
 GAGAGGTTCC CATTAAGGAT GTCGAGGCGG GGAATGGTGA GGAAGAGTCG GGCATGGGTG 780
 50 CTGGAGAAGA AGGAGCGGCA CAGGCGCCAG GGCAGGAAG TCAGACCTGA CACCCAGTAC 840
 ACCGGCCGCA AGCGCAAGCC CCGCTTCTAA GTCAACACGC GGTTCCTGGAA AGGCACTTGC 900
 55 CTCTGCACTT TTCTATATTG TTCAGCTGAC AAAGTAGTAT TTTAGAAAAG TTCTAAAGTT 960
 ATAAAAATGT TTTCTGCAGT AAAAAAAAAA TTCTCTGGGC CGGGCGTGGT GGCTCACACC 1020
 60 TGTAATCCCA GCACCTTGGG AGGCTGAGGT GGGAGGATCA TTTGAGGCCA GGAGTTTGAG 1080

ACCTGCCTGG GCAACATAAT GAAACTTCCT TTCCAGGGAG AAAAAAAAAA AAAAAAAAAA 1140

A 1141

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(2) INFORMATION FOR SEQ ID NO: 55:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1560 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TCCTTCTCTG GGGCGGTTCG GTTGGCAGCG GATGCGGGAA GCCGGACTCT GGGCGTCATG 60
20 TACTACAAGT TTAGTGGCTT CACGCAGAAG TTGGCAGGAG CATGGGCTTC GGAGGCCTAT 120
AGCCCGCAGA TTNAAGCCT GTGGTTTCCA CAGAAGCACC ACCTATCATA TTTGCCACAC 180
CAACTAACT GACCTCCGAT TCCACAGTGT ATGATTATGC TGGGAAAAAC AAAGTTCCAG 240
25 AGCTACAAAA GTTTTCCAG AAAGCTGATG GTGTGCCCGT CTACCTGAAA CGAGGCCTGC 300
CTGACCAAAT GCTTTACCG ACCACCATGG CGCTGACTGT GGGAGGGACC ATCTACTGCC 360
30 TGATCGCCCT CTACATGGCT TCGCAGCCCA AAAACAAATG AGTTAGGCTG CAGAGGACTG 420
GTTTGTMTT TGGCATAAAC CCTTTGAAGT TCCTTTTCA TTGTTAAATT AAAATTTT 480
TTTTTACTTG GATGGCTTAA CATTTTGCA AGAAAAATAG GAAGATATGA AGATGATGTT 540
35 TTGGTTTGT TATGAAATGC ATATGGCTTG TCAGAGCTCA TTCGACAGTT AAAGCCATTG 600
TTTAAAGAAA CGTGCTTTG CTCTGTGTT GTGCTCCTGA TTCCCTGGA GGTCTCGGAT 660
40 GAAGGCTGAA CACAGGCTTG TTAATGTCAG TCTGTGCTGA GGACCTCAGG GACTTGAGGT 720
TGCATTTTGT AGCATGGGGT GCAGGAGCCT TTCTGGATTT GGATGTGGCT ATGGAAAGAA 780
CACAGAAGCC AAGGTCATGT GCATGAAATG AGGAGTTTGA GTTAGTCACC TCGGGGATTT 840
45 TTTCCATTT GCAGTAAAT GTTAAATTAA TGTAGCCTGC CTCTATTGT TGGGCAGGTA 900
ATTTCAAAGG GTTATTTGCC TCATCTCCTA TCTTTAGTGA AATCTTATGT GTAATTGTGT 960
50 GTATTTATTC CACCGTGGGA ACAGAGAATA CCTGTTTAGT GTTGCACTTT AGACTGGTGT 1020
CTGTTTGTGTT AATGCAGCTG TGCCACAAAT TCTCCTTTAT CTTTAAAAA TGTATAGCT 1080
TTAAATTTTG ATTTATTTTG ACTGTGGAAT AAATACATGA ATGAAAAATT TTAAGTTTGA 1140
55 AGTTCTTTGA ATGACCTTC AGAGTAATTT CAGAACACCA GCAGCATCTT AAACCTGAGT 1200
CTAATTTCTT TCTGTTAAT TAGGCACCAG ATAATCTTTA TAAATGGTC TTAAAGCTA 1260
60 GTAATAGGAG CTTAATGGCA ATKGATGATT ACCACAKGGT TTTTATAAAA AACCTGCCTG 1320

5 CCCCTWAGTG AAAGGTACCT GTAACYCACA GTYCATTAG AACTAATTT CCTYTGCYGT 1380
 CATGATTGGK AGACTTCACT TACCCTATAT TAATTTTGAA AAAAGGTGGA ATTTTATTAT 1440
 ATATGAAGGA ATAGTTTGTA TCTTACCATA GCACAGAACA GTGACCTCTT GCTCAGGATA 1500
 AGATGTGGTG ATTTGAAAAT ACTCATAGTA GCCTTGCACT GATACCTCTC TCNCTCTCTC 1560

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(2) INFORMATION FOR SEQ ID NO: 56:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1507 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GGAACGCAGA GCGGAGCGTG GAGAGCGGAG CGAAGCTGGA TAACAGGGGA CCGATGATGT 60
 25 GGGGACCATC AGTTCTGCTG CTTCTGTTGC TACTGAGGCA CGGGGCCAG GGAAGCCAT 120
 CCCCAGACGC AGGCCCTCAT GGCCAGGGGA GGTGCACCA GGCGGCCCC CTGAGCGACG 180
 CTCCCCATGA TGACGCCCAC GGGAACTTCC AGTACGACCA TGAGGCTTTC CTGGGACGGG 240
 30 AAGTGCCAA GGAATTCGAC CAACTCACCC CAGAGGAAAG CCAGGCCCGT CTGGGCGGA 300
 TCGTGGACCG CATGGACCGC GCGGGGACG GCGACGGCTG GGTGTGCTG GCCGAGCTTC 360
 35 GCGCGTGGAT CCGGCACACG CAGCAGCGGC ACATACGGGA CTCGGTGAGC GCGGCCTGGG 420
 ACACGTACGA CACGACCGC GACGGGCGTG TGGTTGGGA GGAGCTGCGC AACGCCACCT 480
 ATGCCCCTA CGCGCCCGGT GAAGAATTTC ATGACGTGGA GGATGCAGAG ACCTACAAAA 540
 40 AGATGCTGGC TCGGGACGAG CGGCGTTTCC GGTGGCCGA CCAGGATGGG GACTCGATGG 600
 CCACTCGAGA GGAGCTGACA GCCTTCCTGC ACCCCGAGGA GTTCCCTCAC ATGCGGGACA 660
 45 TCGTGATTGC TGAAACCCTG GAGGACCTGG ACAGAAACAA AGATGGCTAT GTCCAGGTGG 720
 AGGAGTACAT CGCGGATCTG TACTCAGCCG AGCCTGGGGA GGAGGAGCCG GCGTGGGTGC 780
 AGACGGAGAG GCAGCAGTTC CGGGACTTCC GGGATCTGAA CAAGGATGGG CACCTGGATG 840
 50 GGAGTGAGGT GGGCCACTGG GTGCTGCCCC CTGCCAGGA CCAGCCCCTG GTGGAAGCCA 900
 ACCACCTGCT GCACGARAGC GACACGGACA AGGAYGGGCG GCTGAGCAAA GCGSAAATCC 960
 55 TGGGTAATTG GAACATGTTT GTGGGCAGTC AGGCCACCAA CTATGGYGAG GACCTGACCC 1020
 GGCACCACGA TGAGCTGTGA GCMCCGNGCA CTGCCACAG CCTCAGAGGC CCGCACAATG 1080
 ACCGGAGGAG GGGCCGCTGT GGTCTGGCCC CCTCCCTGTC CAGGCCCCGC AGGAGGCAGA 1140
 60

TGCAGTCCCA GGCATCCTCC TKCCCCTGGG CTCTCAGGGA CCCCCTGGGT CGGCTTCTGT 1200
 CCTGTGACCA CCCCCAACCC CAGGGAGGGG CTGTCATAGT CCCAGAGGAT AAGCAATACC 1260
 5 TATTTCTGAC TGAGTCTCCC AGCCCAGACC CAGGGACCCT NGGCCCAAG CTCAGCTCTA 1320
 AGAACCGCCC CAACCCCTCC AGCTCCAAAT CTGAGCCTCC ACCACATAGA CTGAAACTCC 1380
 CCTGGCCCCA GCCCTCTCCT GCCTGGCCTG GCCTGGGACA CCTCCTCTCT GCCAGGAGGC 1440
 10 AATAAAAGCC AGCGCCGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
 AAAAAAN 1507

15

(2) INFORMATION FOR SEQ ID NO: 57:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAATTCGGCA CGAGCAGTGT CCAACACTGT AGCTGGTGCC TGCCAGGTTT CCAGTGGCTG 60
 30 GGGTCACCAG GTCTGAAGAG AGATGTGCTG GCTGCGGGCA TGGGSCCAGA TCYTCTTGCC 120
 AGTTTTCTTC TCCYTCTTTC TCATCCAATT GCTTATCAGC TTCTCAGAGA ATGGTTTTAT 180
 CCACAGCCCC AGGAACAATC AGAAACCAAG AGATGGGAAT RAAGAGGAAT GTGCTGTAAA 240
 35 GAAGAGTTGT CAATTGTGCA CAGAAGATAA GAAATATATG ATGAATAGAT AATTGAAAAG 300
 AGATCCTCCA GAAAGAGCAG AAGGAAGTTT CTCAATGGC TTCCTTCAGG ATTTTAATCA 360
 40 TCCTTACAGC CTCTTTGAGA ATGATTGAAC TTCCAAATTC CCTGAAGTTA AAATTTTAAA 420
 TTCTATTAAA CATTTTTCG AGTAAAAAA 450

45

(2) INFORMATION FOR SEQ ID NO: 58:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGCACGAGAC CCATTGAGCA GAAGGAGGCC AGGTGGGAAA GTCCTGGGA AGAGCAGCCA 60
 GACTGGACAC TGGGCTGCTT GAGTCCTGAG TCACAATTCA GAATTCCTGG GTCCTCTGGG 120
 60

	TGCATTCTAT CATTCAGTT GAAAGTTTGC TTCCTTCCAG TCATGTGGCT CTTCATTCTA	180
	CTCTCCTTGG CTCTCATTTT AGATGCCATG GTCATGGATG AAAAGGTCAA GAGAAGCTTT	240
5	GTGCTGGACA CGGCTTCTGC CATCTGCAAC TACAATGCCC ACTACAAGAA TCACCCCAA	300
	TACTGGTGCC GAGGCTATTT CCGTGA CTAC TGCAACATCA TCGCCTTCTC CCCTAACAGC	360
10	ACCAATCATG TGGCCCTGAA GGACACAGGG AACCAGCTCA TTGTCACTAT GTCCTGCCTG	420
	AACAAAGAAG ACACGGGCTG GTACTGGTGT GGCATCCAGC GGGACTTTGC CAGGGATGAC	480
	ATGGATTTTA CAGAGCTGAT TGTAAGTGAC GACAAAGGAA CCTGGCCAAT GACTTTGGTC	540
15	TGGGAAAGAC TATCAGGCAC AAAACCAGAA GCTGCAAGGC TCCCAAAGTT GTCCGCAAGG	600
	CTGACCGCTC CAGGACGTCC ATTCTCATCA TTTGCATACT GATCACGGGT TTGGGAATCA	660
20	TCTCTGTAAT CAGTCATTTG ACCAAAAGGA GGAGAACTCA AAGGAATAGA AGGGTAGGCA	720
	ACACTTTGAA GCCCTTCTCG CGTGTCTGTA CTCCAAAGGA AATGGCTCCT ACTGAACAGA	780
	TGTGACTGAA GATTTTTTTA ATTTAGTTCA TAAAGTGATG CTACAACAGA ATAATCACCA	840
25	TGACAACTGG CCCCACACCT CAGAGACTGA TTCTGATCTC CCAGGAATTC TGAAGGTCCC	900
	TCTATCCTTG ACAACAATCA TTTGCAGCCA GGTAGCAACG GCAGTAGTCA GAGGAGCTAT	960
30	GATAGACCAC ACCCAAGCAA GGCTGCCCTC AAATAACATC TCAAGATCTT AGTTCTTATG	1020
	CATTCCATCA GTCAGAAGTG AAGAAGAGGT GGAGAATCTG GATTGGGGAC CAGGAAATCA	1080
	CTTGATTTTT GTTAGCCAAT AAATTCCTAG CCAGTGTGTA ATGAAAAAA AAAAAAAA	1140
35	AAAAAA	1147

40 (2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

50	GGCAGAGGCT CCTCAGAAGG GCGTGGGCTC TCCAGTCTTC CACAGTCCCC ACCATGCCCT	60
	GTTCCTTAC CGCTGACGTA GCTCACCCAT CTTTACTTIG CCTGGCTAAG ATGCATGGCA	120
	TYWCATTTCC TCCTTGTTC ACTGCAGTCA GTCCCTCACT GCCCCATCT CTGGAAGAG	180
55	GAGCATAAGC TTTGCAAGGT CAGCCACTTC TCTGGGTCA CACTAGTTAC ATCAAGACAG	240
	GACTCCAGCT CATATGTGCC AGTGCAGACA CTCTCATCC ACCTGGGGCC CTGGGCTTGG	300
60	GACCTGGYTC CTGACAGC AGARGACCG GAGGCTGAGA GGAGCTTGGC GTTGTGTCAT	360

5 AGTCACCTGG CCAGARGGAA CGTGAGCCCC TCCCAAGCTG CAGARGGARG GARCARGCGT 420
 GGCTGTGAGC ACCGAGGTAG CAGAGAATTA ACATTCTTGT CAGCAGAGAA TGAAGCAGGA 480
 ATATAATTAA AACTTTGCCC TTGGAATAGC TGATTCAATT GAATTTTATT CCACACGTTT 540
 GAAAGAGGAA AGAAAATGTG AAGACTTGCA GCCTGGTTCT CGCCTGGCCT GGGCTGGCCC 600
 10 AGCTGTCAGG CCCGGTTCCT TTCTGAGCAT TCAGTCCACT GATGTTGACT GAGGGCCAGG 660
 AGAGACCCTC AGCAGGGTAT TACCATATCA GCCTCCTATC GCTGCTGGGA GAAATTACCA 720
 TGAATTCAGT GGCTTAAAC AACACACGAG CCTCTCTGAG CCTACCCTGG CTCAGGA 777
 15

(2) INFORMATION FOR SEQ ID NO: 60:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

30 AAGANTGATT TTCCTTACTC TCCAAAGCGT CAGCATTTTG AAGTTTCTTT TATGAAAGTG 60
 GGGGCAAGAA TCAGGGTGAA AATGAGTGTA AACAAAGCCC ATCCTGTGGT CAGCACCCAC 120
 TGGAGGTGGC CAGCAGAGTG GCCTCAGATG TTCCTGCACC TGGCCCAGGA GCCCAGGACA 180
 35 GAGGTCAAAT CTAGGCCCTT TGGTCTGGCT GGATTCATCA GGCAAGATTC GAAAACAAGA 240
 AAACCTCTAG AACAGAAAC AATCATGTCT GCAGCAGATA CGGCACTGTG GCCCTATGGC 300
 CATGGCAATC GTGAGCACCA AGAGAATGAG TTACAGAAAT ATCTCCAATA CAAAGACATG 360
 40 CATCTCCTGG ACAGTGGACA GTCGCTGGGA CACACACACA CACTTCAAGG CTCACACAAC 420
 CTAACAGCCT TAAATATCTG AAGAAACAGA ATCAGCAGAT TAAGTCAGCA GAGGGAGAGG 480
 45 TAGGCTGAAG CAGCAGGAGG CCAATTTTAT ATCCCACAGA TTTTTTTAAA AATGACTCCC 540
 CAGCAAGGGG TGGGGAGAAA GCCACTGATT TAGGAGAGTT CTTGGCTCAG CCAACCACTG 600
 CGTTATCTA CACGTTTAC AAAGGCACRG AAGTAGAGAG GGGCTGCACT CACGACCCTC 660
 50 CCCAGGGCCC GCACAGCCAG ACACGGTGGG TTCTTCCITT TTCCCTTCTG GCCTTGGTGG 720
 AATTCCTACC ACGGTGGCCT CTGCCTTTGG GACAATGCCT TCATGCTCAT CCCCGGGTCA 780
 55 AGGATGGAGT CTGTTACCAT TTTCCAGGGG AAATTCCAAG GACCAGCCCC GCCTCATTAC 840
 GTTCACCCCA CAGGAAGGTG ATCTGGAAG CCTGTAAACA CGTACTCTGG GTGGCTGAGT 900
 GGTGTCACCA AGCTGCTTTT GTGCAGGGCT GAAGCACAGA CAAGAGGGCA GGCAGCTGCC 960
 60

GGAGGCCTGA AGTGGGGAGA GATCCCCGCA GGCCTGCAGG AGCCAGGGAG AACCTCCAAC 1020
 TGGATCTAAA CTGTGGGACA GCCCAGGCGT GCCCCTCTTC ACATGGCTCC CAGGCTCCCT 1080
 5 CAAAGCCCTT CCCAGGCCCT GCAGGAAGAG AGGGAGGGTG AGGAGAGGCA GGGAGGGCAG 1140
 AGGTGCGCTG AAAGCCTGGG CTCGAACTC CCTCAGCAGA GCTTTAAAGT G 1191

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(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 1580 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCCCGCCCC CGCCACGAA GGAAGTGGCT GCTGCTCCGG CGCGGACCCA GAGCCGGTTC 60
 GGCGGTGCA CTGCCCAGAG TCCGCGGCCG GGCGCGGGAG GAGCCAAGCC GCCATGGCCT 120
 25 ACCACAGCTT CTGCTGGAG CCCATCAGCT GCCACGCTG GAACAAGGAC CGCAGCCAGA 180
 TTGCCATCTG CCCCACAAAC CATGAGGTGC ATATCTATGA AAAGAGCGGT GCCAAATGGA 240
 30 CCAAGGTGCA CGAGCTCAAG GAGCACAACG GGCAGGTGAC AGGCATCGAC TGGGCCCCCG 300
 AGAGTAACCG TATGTGTACC TCGGCACAG ACCGCAACGC CTACGTGTGG ACGCTGAAGG 360
 GCCGCACATG GAAGCCCACG CTGGTCATCC TCGGATCAA CCGGGCTGCC CGCTGCGTGC 420
 35 GCTGGGCCCC CAACGAGAAC AAGTTTGTGT TGGGAGCGG CTCTCGTGTG ATCTCCATCT 480
 GTTATTTGCA GCAGGAGAAT GACTGGTGGG TTTGCAAGCA CATCAAGAAG CCCATCGCT 540
 40 CCACGTCCT CAGCCTGGAC TGGCAGCCCA ACAATGTGCT GCTGGCTGCC GGCTCCTGTG 600
 ACTTCAAGTG TCGATCTTT TCAGCCTACA TCAAGGAGT GGAGGAACGG CCGGCACCCA 660
 CCCCCTGGGG CTCCAAGATG CCCTTTGGGG AACTGATGTT CGAATCCAGC ACTAGCTGCG 720
 45 GCTGGGTACA TGGCGTCTGT TTCTCAGCCA GCGGAGCCG CGTGGCCTGG GTAAGCCACG 780
 ACAGCACCGT CTGCCTGGCT GATGCCGACA AGAAGATGGC CGTCGCGACT CTGGCCTCTG 840
 50 AAACACTACC ACTGCTGGCG CTGACCTTCA TCACAGACAA CAGCCTGGTG GCAGCGGGCC 900
 ACGACTGCTT CCCGGTGTG TTCACCTATG ACGCCGCCGC GGGGATGCTG AGCTTCGGCG 960
 GGCGGCTGGA CGTTCCTAAG CAGAGCTGCG AGCGTGGCTT GACGGCCCGC GAGCGCTTCC 1020
 55 AGAACCTGGA CAAGAAGCG AGCTCCGAGG GTGGCACGGC TCGGGCGCG GGCCTAGACT 1080
 CGCTGCACAA GAACAGCGTC AGCCAGATCT CGGTGCTCAG CGGCGGCAAG GCCAAGTGCT 1140
 60 CGCAGTCTG CACCACTGGC ATGGATGGCG GCATGAGTAT CTGGGATGTG AAGAGCTTGG 1200

5 AGTCAGCCTT GAAGGACCTC AAGATCAAAT GACCTGTGAG GAATATGTTG CCTTCATCCT 1260
 AGCTGCTGGG GAAGCGGGGA GAGGGGTCAG GGAGGCTAAT GGTGCTTTG CTGAATGTTT 1320
 CTGGGGTACC AATACGAGTT CCCATAGGGG CTGCTCCCTC AAAAAGGGAG GGGACAGATG 1380
 GGGAGCTTTT CTTACCTATT CAAGGAATAC GTGCCCTTTT CTTAAATGCT TTCATTTATT 1440
 10 GAAAAAAAAA AAAAATGCCC CCAAAGCACT ATGCTGGTCA TGAATGCTT CAAAATGTGG 1500
 AGGTAATAAA ATGCAACTGT GTAAAAAAAA AAAAAAAAAA AAATGACCCT CGCGATCTAG 1560
 AACTAGNCGG ACGCNTGGGT 1580

20 (2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1117 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

30 GGCACGAGGC GCGATGCAGC ACAGGCTAGA GGCTGCGCAA SGCGGGGGCC CGCCCCTGGG 60
 ACCCTCCGGG CCGGGCGGTT TGGCCCTTCA GCGCCCGGGC GTCGGGGCGG TAAAAGGCCG 120
 GCAGAAGGGA GGCACCTGAG AAATGTCTTT CCTCCAGGAC CCAAGTTTCT TCACCATGGG 180
 35 GATGTGGTCC ATTGGTGCAG GAGCCCTGGG GGCTGCTGCC TTGGCATGTC TGCTTGCCAA 240
 CACAGACGTG TTTCTGTCCA AGCCCCAGAA AGCGGCCCTG GAGTACCTGG AGGATATAGA 300
 CCTGAAACA CTGGAGAAGG AACCAAGGAC TTTCAAAGCA AAGGAGCTAT GGGAAAAAAAA 360
 40 TGGAGCTGTG ATTATGGCCG TGCGGAGGCC AGGCTGTTTC CTCTGTCGAG AGGAAGCTGC 420
 GGATCTGTCC TCCCTGAAAA GCATGTTGGA CCAGCTGGGC GTCCCCCTCT ATGCAGTGGT 480
 45 AAAGGAGCAC ATCAGGACTG AAGTGAAGGA TTTCCAGCCT TATTTCAAAG GAGAAATCTT 540
 CCTGGATGAA AAGAAAAAGT TCTATGGTCC ACAAAGGCGG AAGATGATGT TTATGGGATT 600
 TATCGTCTG GGAGTGTGGT ACAACTTCTT CCGAGCCTGG AACGGAGGCT TCTCTGGAAA 660
 50 CCTGGAAGGA GAAGGCTTCA TCCTTGGGGG AGTTTTCGTG GTGGGATCAG GAAAGCAGGG 720
 CATTCCTCTT GAGCACCGAG AAAAAGAATT TGGAGACAAA GTAAACCTAC TTTCTGTTCT 780
 55 GGAAGCTGCT AAGATGATCA AACCACAGAC TTTGGCCTCA GAGAAAAAAT GATTGTGTGA 840
 AACTGCCCAG CTCAGGGATA ACCAGGGACA TTCACCTGTG TTCATGGGAT GTATTGTTTC 900
 60 CACTCGTGTC CTAAGGAGT GAGAAACCCA TTTATACTCT ACTCTCAGTA TGGATTATTA 960

ATGTATTTTA ATATTCTGTT TAGGCCCACT AAGGCAAAAT AGCCCCAAA CAAGACTGAC 1020
 AAAAATCTGA AAAACTAATG AGGATTATTA AGCTAAAACC TGGGAAATAG GAGGCTTWAA 1080
 5 ATGACTGCCM GCTGGTG CRT GCTCACACTT GGCCAC 1117

10 (2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

20 CCCACGCGTG CKGGCGCCTG GCAGCCACCG CCTGGGAGGT TACTGTAAGG CCCGCAGCTC 60
 CCGCCAGCTC CCGCGGACTS CTGCCGCCTC CTTACCATGA AGCCAGTAAG TCGTCGCACG 120
 CTGGACTGGA TTTATTCACT GTTGCTGCTT GCCATCGTTT TAATCTCCTG GGGCTGCATC 180
 25 ATCTATGCTT CGATGGTGTC TGCAAGACGA CAGCTAAGGA AGAAATACCC AGACAAAATC 240
 TTTGGGACGA ATGAAAATTT GTAACCTCTC TGGATTTAAT TATCTGAAAA TACAGTTCTT 300
 30 TCCCTCATGC TTATGTAGAT ATAAAAATAA AATTCATAAT GCAAAAAAAA AAAAAAAAAA 360
 G 361

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(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1668 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGCAGGAGT CTGCCAAGCT ATAGACCATG GCTGTGAACA CATTTGTGTG AACAGTGACG 60
 ACTCATACAC GTGCGAGTGC TTGGAGGGAT TCCGGCTCGC TGAGGATGGG AAACGCTGCC 120
 50 GAAGAAGGAT GTCTGCAAAT CAACCCACCA TGGCTGCGAA CACATTGTGT TTAATAATGG 180
 GAATTCCTAC ATCTGCAAAT GCTCAKAGGG ATTTGTTCTA GCTGAGGACG GAAGACGGTG 240
 55 CAAGAAATGC ACTGAAGGCC CAATTGACCT GGTCTTTGTG ATCGATGGAT CCAAGAGTCT 300
 TGGAGAAGAG AATTTTGAGG TCGTGAAGCA GTTTGTCACT GGAATTATAG ATTCCTTGAC 360
 AATTTCCTCC AAAGCCGCTC GAGTGGGGCT GCTCCAGTAT TCCACACAGG TCCACACAGA 420
 60

GTTCACTCTG AGAAACTTCA ACTCAGCCAA AGACATGAAA AAAGCCGTGG CCCACATGAA 480
 ATACATGGGA AAGGGCTCTA TGA CTGGGCT GGCCTGAAA CACATGTTTG AGAGAAGTTT 540
 5 TACCCAAGGA GAAGGGGCCA GGCCCTTTCC ACAAGGGTGC CCAGAGCAGC CATTGTGTTC 600
 ACCGACGGAC GGGCTCAGGA TGACGTCTCC GAGTGGGCCA GTAAAGCCAA GGCCAATGGT 660
 ATCACTATGT ATGCTGTGG GGTAGGAAAA GCCATTGAGG AGGAAC TACA AGAGATTGCC 720
 10 TCTGAGCCCA CAAACAAGCA TCTCTTCTAT GCCGAAGACT TCAGCACAAT GGATGAGATA 780
 AGTGAAAAAC TCAAGAAAGG CATCTGTGAA GCTCTAGAAG ACTCCGATGG AAGACAGGAC 840
 15 TCTCCAGCAG GGGAAGTCC AAAAACGGTC CAACAGCCAA CAGTGCAACA CAGATATCTG 900
 TTTGAAGAAG ACAATCTTTT ACGGTCTACA CAAAAGCTTT CCCATTCAAC AAAACCTTCA 960
 GGAAGCCCTT TGGAAGAAAA ACACGATCAA TGCAAATGTG AAAACCTTAT AATGTTCCAG 1020
 20 AACCTTGCAA ACGAAGAAGT AAGAAAATTA ACACAGCGCT TAGAAGAAAT GACACAGAGA 1080
 ATGGAAGCCC TGGAAAATCG CCTGAGATAC AGATGAAGAT TAGAAATCGC GACACATTTG 1140
 25 TAGTCATTGT ATCACGGATT ACAATGAACG CAGTGCAGAG CCCCAAAGCT CAGGCTATTG 1200
 TTAAATCAAT AATGTTGTGA AGTAAACAA TCAGTACTGA GAAACCTGGT TTGCCACAGA 1260
 ACAAAGACAA GAAGTATACA CTAATTGTA TAAATTTATC TAGGAAAAAA ATCCTTCAGA 1320
 30 ATTCTAAGAT GAATTTACCA GGTGAGAATG AATAAGCTAT GCAAGGTATT TTGTAATATA 1380
 CTGTGGACAC AACTTGCTTC TGCCTCATCC TGCCTTAGTG TGCAATCTCA TTTGACTATA 1440
 35 CGATAAAGTT TGCACAGTCT TACTTCTGTA GAACACTGGC CATAGGAAAT GCTGTTTTTT 1500
 TGTATGAC TTTACCTTGA TATATGTATA TGGATGTATG CATAAAATCA TAGGACATAT 1560
 GTACTGTGG AACAGTTGG ATTTTTTATA CAATATTAAA ATTCACCACT TCAGAGRAAA 1620
 40 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAANAAAA 1668

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(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GGGTCGACCC ACGCGTCCGC CCAAGCGTCC GGATGGCTGC GCTGTGCTG AGACACGTTG 60
 GTCGTCATTG CCTCCGAGCC CACTTTAGCC CTCAGCTCTG TATCAGAAAT GCTGTTCTTT 120
 60 TGGGAACCAC GGCCAAAGAA GAGATGGAGC GGTCTCGAA TAAGATATA GGTTCAAACC 180

5 GTCTCTGTGTC TCCCACATT ACTATCTACA GTTGGTCTCT TCCCATGGCG ATGTCCATCT 240
 GCCACCGTGG CACTGGTATT GCTTTGAGTG CAGGGGTCTC TCTTTTGGC ATGTCGGCCC 300
 TGTACTCCCC TGGGAACTTT GAGTCTTATT TGGAACTTGT GAAGTCCCTG TGTCTGGGGC 360
 CAGCACTGAT CCACACAGCT AAGTTTGCAC TTGTCTTCCC TCTCATGTAT CATACCTGGA 420
 10 ATGGGATCCG ACACTTGATG TGGGACCTAG GAAAAGGCCT GAAGATTCCC CAGCTATAACC 480
 AGTCTGGAGT GGTGTCTCTG GTTCTTACTG TGTGTCTCTC TATGGGGCTG GCAGCCATGT 540
 GAAGAAAGGA GGCTCCCAGC ATCATCTTCC TACACATTAT TACATTCACC CATCTTTCTG 600
 15 TTTGTCAATC TTATCTCCAG CCTGGGAAAA GTTCTCCTTA TTTGTTTAGA TCCTTTTGTA 660
 TTTTCAGATC TCCTTGGAGC AGTAGAGTAC CTGGTAGACC ATAATAGTGG AAAAGGGTCT 720
 20 AGTTTTCCCC TTGTTTCTAA AGATGAGGTG GCTGCAAAAA CTCCCCTTTT TTGCCCACAG 780
 CTTGCCTACT CTCGGCCTAG AAGCAGTTAT TCTCTCTCCA TATTGGGCTT TGATTTGTGC 840
 TGAGGGTCAG CTTTGGCTC CTTCTTCTG AGACAGTGA AACAATGCCA GCTCTGTGGC 900
 25 TTCTGCCCTG GGGATGGGCC GGGTGGGGG GTGGGTGGT GAGGCTTTGG GTGCCACTGC 960
 CTGTGGGTG CTGGCTTAA GGACAATTCT CTTTATTGGT GAGAGCCCAG GCCATTAAACA 1020
 30 CCTACACAGT GTTATTGAAA GAAGAGAGGT GGGGGTGGAG GGGAAATTAGT CTGTCCCAGC 1080
 TAGAGGGAGA TAAAGAGGGC TAGTTAGTTC TTGGAGCAGC TGCTTTTGAG GAGAAAATAT 1140
 ATAGCTTTGG ACACGAGGAA GATCTAGAAA ATTATCATTG AACATATTAA TGGTTATTTT 1200
 35 TTTTCTTGG ATTTCCAGAA AAGCCTCTTA ATTTTATGCT TTCTCATCGA AGTAATGTAC 1260
 CCTTTTTTTC TGAAACTGAA TTAATACTC ATTTTATCTT TGAAAAAAA AAAAAAACC 1320
 40 TNGGGGGGGG CCCCAGACCC NAATTGGCCC TAT 1353

45 (2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1011 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

55 CGGAAGAAAG CAGCCATCCA GACATTTCAG AACACGTACC AGGTGTTAGC TGTGACCTTC 60
 AATGACACAA GTGATCAGAT TATTTCTGGT GGAATAGACA ATGATATCAA GGTCTGGGAC 120
 TGCGCCAGAA CAAGCTAACC TACACCATGA GAGGCCATGC AGATTCACTG ACTGGCCTGA 180
 60

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GTTTAAGTTC TGAAGGCTCT TATCTTTTGT CCAATGCAAT GGACAATACA GTTCGTGTCT 240
 GGGATGTCCG GCCATTTGCC CCCAAAGAGA GATGTGTAAA GATATTTCAA GGAAATGTGC 300
 5 ACAACTTTGA AAAGAACCTT CTGAGATGTT CTGTGTCACC TGATGGAAGC AAAATAGCAG 360
 CTGGCTCAGC CGACAGGTTT GTTTATGTGT GGGATACCAC AAGCAGGAGA ATATTGTATA 420
 AGCTGCCCCG CCATGCTGGC TCCATCAATG AAGTGGCTTT CCACCCTGAT GAGCCCATCA 480
 10 TTATCTCAGC ATCGAGTGAC AAGAGACTGT ATATGGGAGA GATTCACTGA AGATATGGAC 540
 TGAAGACTC CAAGGCCGCT TGTCTTTGAG ACCTCAGACT GCATAAGTGA TGCCAAATGT 600
 15 TGGATGTCCA GGYTAGCACC CTCCTTCAG ATGACCATTG CTAGCAAGAA ACAGGAGGCG 660
 GTGGCCATAT TCCAAAAACC ACTTCTGTCC CATTTACCA GGATGACTAA GGCAAGCTCC 720
 CTGTGGCCTC TAAAAACCAC CTGCCAGATT TCAGGGACTG TTTTTTTTTT TCTTTTCTT 780
 20 TTTTCTGTT TTCTAATGCA GGGCCAATGT GACAAATTG TTGGTTGGGA TTTTTTTTTT 840
 TTTTGTAAAC TGGCTGTAT GATATTTTCT TTCGTATTT CTCTATATCA TTTTGTATTA 900
 25 AAAGCCAAAT AGATGCCTTT TTACAAGARM AAAAAAAAAA AAAAAAAAAA NNAAAAAAAA 960
 CTGGGAGGGG GGGCCCGTA CCCAAATCGC CGGATATGAT CGTAAACAAT C 1011

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(2) INFORMATION FOR SEQ ID NO: 67:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1193 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GGGCGGGCGG TGGCACTGC GGGCGCATCC CTGCCCCGGC GCCGTCCGTG CCGCGGGAC 60
 CTGACAGCCG GGTGAGAGG CGAACTGTGC TCAGGCCCGG GCTGGACGCA GAGCCAGAGC 120
 45 TGTCCCAGA GGAGCAGAGG GTCCTGAAA GGAAGCTGAA AAAGGAACGG AAGAAAGAGG 180
 AGAGGCAGCG TCTGCGGGAG GCAGGCCTTG TGGCCAGCA CCCGCCTGCC AGGCGCTCGG 240
 50 GGGCCGAAT GGCCTGGGAC TACCTCTGCA GATGGGCCCA AAAGCACAAG AACTGGAGGT 300
 TTCAGAAGAC GAGGCAGACG TGGCTCCTGC TGCACATGTA TGACAGTGAC AAGGTTCCTG 360
 ATGAGCACTT CTCCACCCTG CTGGCCTACC TGGAGGGGCT GCAGGGCCCG GCCCGAGAGC 420
 55 TGACGGTGCA GAAGCGGAA GCCTGATGCG GGAGCTGGAT GAGGAGGGCT CTGATCCCCC 480
 CCTGCCGGGG AGGGCCAGC GCATCCGACA GNTGCTGCAG CTGCTCTCCT AGTGGGTCA 540
 60 GCGCGGGCGG GGGCGCTGC CCAGTGCAGG GCTGCCTCAG ACCACACAGG GTGCAGCTCC 600

TCCGGCCGGT GGGGCCGGGT TCACCAGCAG GGCAGCGGCT GAGCAAGGGC TTTCAGCTCC 660
 TCCGGTGGTG GGGGCCGGGA TCACCAGCAC CAGAGCCTCG CAAGGGCCCC TTCCCTCCTC 720
 5 CAGACCCTCC TTGGCCGGTG ACGCTGTGAC AGTGATGGCA GGTTCAGTGC CTTCAGCGCA 780
 GAGCGTGGAT GCTCTGGAAT CACCCGACC CCTGGCCTTG GAGGGACCCT CCAGCCCCAG 840
 10 GAATCTGCTT TGGAGGAAA TGTCTATTTT TCTACCGGA ATATTTTAGA GATTGGGGCA 900
 TGCTGGCTCC TCCC GCCAGC TGCAAACCTG CACCTCCGC CTGATTCCCG ATCCCCCTGC 960
 GTGGGCCGCA TTCCTGGTCC CTGCCTGCG TCCATCGAGG GGCCTGGCTG TGGCCTGTTT 1020
 15 TCCTTTGACC CCACACAGCG TCATTGCGGG TCATGGGGAG CCCCTGGTGG GAGCTTGTGG 1080
 AGTCGGATCA CGTACCTGTG CAGAAACCGC CTCTGTGGCT GCATTTGAAA TAAAACCCGA 1140
 20 CCCAGCAGCA AAAAAAAAAA AAAAAANCNC NAGGGGGGGC CCGGNACCCA ATT 1193

25 (2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

35 GAATTCGGCA CGAGTTGGCA CATGATGCAA AATGCATTTT TCAGAGTAGA TTGCAGTCAA 60
 AAATGTTGGA AACTACTAAG CATGTGCARA TAGCATGCAT GCTGCTGCTG ACCTGCCAGA 120
 TATTTCTCCC TTCCTCCCTT TCTCCCTCAT TTATTCATTC ATTAAGTGAT TCATTCATCC 180
 40 CATTAAAAAA ATTATATGTA TGTTTGTGTC AAAGCACCCT ACTCAAGGCT GCGGGGTACA 240
 AAAGTATATC AGAAGCCTTG GGCTTGACM WACTTCTCTG TAGTAGTGCT AGATTTGTGT 300
 45 GGATCTGCCA CACTTACTCC AGGCCTCTTG TGACCTGTGC TTTGCATTAA TCTCTTAGGC 360
 TAAGCCACAT ACCTTTTCAT TATACAATCT TTGCTGATGC TAAGGACAGA TTCCAAAGTG 420
 CCTCCTTAT AATTTTGTGA TTTAATGCAA AGTGTAATCA AGAATAGGCC ATTGTTAGGT 480
 50 CAATTGCTTT TCTGTATTTA TCTTTTCAAA CAATAAATAA TCAGTGGGAT GAAAAAGGGC 540
 CGGAAAAAAA AAAAAAAAAA 560

55

(2) INFORMATION FOR SEQ ID NO: 69:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

	CGGACNGAGC CGCCGCCGGG CACTTCCTGT GGAGGCCGCA GCGGGTGCGG GCGCCGACGG	60
10	GCGAGAGCCA GCGAGCGAGC GAGCGAGCCG AGCCGAGCCT CCCGCCGTCTG CCATGGGCCA	120
	GAACGACCTG ATGGGCACGG CCGAGGACTT CGCCGACCAG TTCCTCCGTG TCACAAAGCA	180
15	GTACCTGCCC CACGTGGCGC GCCTCTGTCT GATCAGCACC TTCCTGGAGG ACGGCATCCG	240
	TATGTGGTTC CAGTGGAGCG AGCAGCGCGA CTACATCGAC ACCACCTGGA ACTGCGGCTA	300
	CCTGCTGGCC TCGTCCTTCG TCTTCCTCAA CTGCTGGGA CANTGACTGG CTGCGTCTTG	360
20	GTGTTGAGCA GGAACATTCGT GCAGTACGCC TGCTTCGGGC TCTTTGGAAT CATAGCTCTG	420
	CAGACGATG CCTACAGCAT TTTATGGGAC TTGAAGTTTT TGATGAGGAA CCTGGCCCTG	480
25	GGAGGAGGCC TGTGCTGCT CCTAGCAGAA TCCCGTTCTG AAGGGAAGAG CATGTTTGCG	540
	GGCGTCCCCA CCATGCGTGA GAGTCCCCC AAACAGTACA TGCAGCTCGG AGGCAGGGTC	600
	TTGCTGGTTC TGATGTTTAT GACCTCCTT CACTTTGACG CCAGCTTCTT TTCTATTGTC	660
30	CAGAACATCG TGGGGCACAG CTCTGATGAT TTTAGTGGCC ATTGGTTTTA AAACCAAGCT	720
	GGCTGCTTIG ACTCTTGTG TGTGGCTCTT TGCCATCAAC GTATATTTCA ACGCCTTCTG	780
35	GACCATTCCA GTCTACAAGC CCATGCATGA CTTCTGAAA TACGACTTCT TCCAGACCAT	840
	GTCGGTGATT GGGGGCTTGC TCCTGGTGGT GGCCTGGGC CCTGGGGGTG TCTCCATGGA	900
	TGAGAAGAAG AAGGAGTGGT AACAGTCACA GATCCCTACC TGCCTGGCTA AGACCCGTGG	960
40	CCGTCAAGGA CTGGTTCGGG GTGGATTCAA CAAACTGCC AGCTTTTATG TATCCTCTTC	1020
	CCTTCCCTC CCTTGGTAAA GGCACAGATG TTTTGAGAAC TTTATTTGCA GAGACACCTG	1080
45	AGAATCAATG GCTTCAGGAC ATGGGTCTC TTCTCCTGTG ATCATTCAAG TGCTCACTGC	1140
	ATGAAGACTG GCTGTCTCA GTGTTTCAAC CTCACCAGG CTGTCTCTTG GTCCACACCT	1200
	CGCTCCCTGT TAGTGCCGTA TGACAGCCCC CATCAAATGA CCTTGGCCAA GTCACGGTTT	1260
50	CTCTGTGGTC AAGGTGGTT GGCTGATTGG TGGAAGTAG GGTGGACCAA AGGAGGCCAC	1320
	GTGAGCAGTC AGCACCAGTT CTGCACCAGC AGCGCCTCCG TCCTAGTGGG TGTTCCTGTT	1380
55	TCTCCTGGCC CTGGGTGGC TAGGGCCTGA TTCGGGAAGA TGCCTTTGCA GGGAGGGGAG	1440
	GATAAGTGGG ATCTACCAAT TGATTCTGGC AAAACAATTT CTAAGATTTT TTGCTTTAT	1500
	GTGGGAAACA GATCTAAATC TCATTTTATG CTGTATTTTA TATCTTAGTT GTGTTTGAAA	1560
60	ACGTTTTGAT TTTTGAAAC ACATCAAAAT AAATAATGGC GTTGTGTGTA AAAAAAAAAA	1620

AAAAAACTC GRGGGGGGC CCGGTACCCA AATCGCC

1657

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(2) INFORMATION FOR SEQ ID NO: 70:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GGCAGGAGCG AAGACCCTGT TCGGACCCTG CCCGATTC AGACTCAGGT AGATCGTCGG	60
CATACCCCTCT ACCGTGGACA CCAGGCAGCC CTGGGGCTGA TGGAGAGAGA TCAGGTATCC	120
CCCAGGGAGT AGGGGCTACC TTGAGGGGAT GATAGACCTC CCCCACTCCC AGTGKCACTC	180
TGGAAATATG AAGGAACTAG GGAGTGAAG AGATTTCAGA GCTGGGGAGA GGAGTTCCTC	240
CCTTCAAAGC CAGCAACTGC CTTTGGGGAA TGTGGGGGG TCTCTCCTTT CTCCTGCTTG	300
TTTRAGGTGG TACACAGTCC CCCCTTCAMC TGGSGGGAAG CTGTNCCGGA CARACTCATC	360
TCAGCTTTCC CTTGGGGCAG GATCGGGGGC AGCAGCTCCA GCAGAAACAG CAGGATCTGG	420
AGCAGGAAGG CCTCGAGGCC ACACAGGGGC TGCTGGCCGG CGAGTGGGCC CCACCCCTCT	480
GGRAGCTGGG CAGCCTCTTC CAGGCCCTTCG TGAAGAGGGA GAGCCAGGCT TATGCCTAAG	540
CTTCATAGCT TCTGCTGGCC TGGGGTGGAC CCAGGACCCC TGGGGCCTGG GTGCCCTGAG	600
TGGTGGTAAA GTGGAGCAAT CCCTTCACGC TCCTTGGCCA TGTCTGAGC GGCCAGCTTG	660
GCCTTTGCCT TAATAAATGT GCTTTATTTT CAAAAA AAAA AAAA T	711

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(2) INFORMATION FOR SEQ ID NO: 71:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 935 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

GGCAGGGT GAAAGCCAGC TAAACCCCAA GTGGAGAAGT GAAAGACATG GTTGTTCCTCA	60
TAAGTTTATT GCTCACATTA TGAAAGAAGC CATAGTCATG AGTGAACCAC TCCCTAGGTT	120
GATAAGGAAA CCAACACGGA AGATCTCTTT CTGGAAGAAG CAGCCAGCCT CGTGAAGGAG	180
CGGCCAGCC GCCGGGCCG AGGGTCGCCT TTTGTTCCGA GTGGCAGCAT TGTCCGTTCC	240

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	CAGACATTCCT CGCCTGGAGC ACGAAGCCAG TATGTTTGCA GACTTTATCG TAGTGACAGC	300
5	GACAGTTCAA CGCTGCCCCG GAAGTCCCCC TTTGTCCGAA ATACTTTGGA AAGACGAACC	360
	CTTCGCTATA AGCAGTCATG CAGGTCTTCC CTGGCTGAGC TCATGGCCCCG CACCTCCCTG	420
	GACTTGGAGC TGGATCTCCA GGCCTCGAGA ACACGGCAGA GGCAGCTGAA TGAGGAGCTC	480
10	TGCGCCCTCC GTGAGCTGCG GCAGCGGTTN GGAGGACGCC CAGCTCCGTG GCCAGACTGA	540
	CCTCCACCCC TGGGTGCTTC GGGACGAGCG GCTCCGTGGC CTGCTGCGGG AGCCGAGCGG	600
15	CAGACAAGAC AGACCAAACCT TGA CTACCGT CATGAGCAGG CGGCTGAGAA GATGCTGAAG	660
	AAGGCCTCCA AGGAGATCTA CCAGCTGCGT GGCAGAGCCA CAAAGAGCCC ATCCAAGTGC	720
	AGACCTTTAG GGAGAAGATA GCATTCTTCA CAAGGCCAAG GATCAACATA CCTCCTCTCC	780
20	CAGCCGACGA CGTCTGATGG AGTGCATTGT GCACATGAAG TATTTATCCA CCTGTTTTAT	840
	TTTCATGAAG TTCTTAGACT AGCTGAATTT GTCTTTAAAA TATTTGTGCA AAGCTATTAA	900
25	TATACACATT TTGTAaaaaa AAAAAAAAAA AACT	935

30 (2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

40	GCAGGGGCGA GGGGYTGGGG ACCGCGGGGC GGACGGGAGC GAGTATGTCC GCTCTGACTC	60
	GGCTGGCGTC TTTGCTCGC GTTGAGGCC GCCTTTTCAG AAGCGGCTGC GCACGGACTG	120
	CTGGAGATGG TGGAGTCCGT CATGCCGGTG GTGGTGTGCA CATGAGCCC CGGTATAGAC	180
45	AGTTCCCCCA GCTGACCAGA TOCCAGGTGT TCCAGAGCGA GTTCTTCAGC GGACTCATGT	240
	GGTTCTGGAT TCTCTGGCGC TTTTGGCATG ACTCAGAAGA GGTGCTGGGT CACTTTCCGT	300
50	ATCCTGATCC TTCCAGTGG ACAGATGAAG AATTAGGTAT CCCTCCTGAT GATGAAGACT	360
	GAAGGTGTAG ACTCAGCCTC ACTCTGTACA AGAGCCAGGT GAGAATTTC AAGATTATCG	420
	ACTTCATATT GCACATTAAA GTTACAAATT AAAGTGGCTT GGTCAAGAAT GARAAAAAA	480
55	AAAAAAAATT GGGGGGGGC CCN	504

60 (2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

10 GAATTCGGCA CGAGGAGGAG GGGAGGCGGG GTAAGTTTGG TGGGAACTC TGTAATTTCC 60
 WTTTCTACTT TCACAGCAAT AGTGCAGAAT CCAGAATGGA TGTCTCTTT GTAGCCATCT 120
 TTGCTGTGCC ACTTATCTTG GGACAAGAAT ATGAGGATGA AGAAAGACTG GGAGAGGATG 180
 15 AATATTATCA GGTGGTCTAT TATTATACAG TCACCCCCAG TTATGATGAC TTTAGTGCAG 240
 ATTTACCAT TGATTACTCC ATATTGAGT CAGAGGACAG GCTGAACAGG TTGGATAAGG 300
 20 ACATAACAGA AGCAATAGAG ACTACCATTA GTCTTGAAAC AGCACGTGCA GACCATCCGA 360
 AGCCTGTAAC TGTGAAACCA GTAACAACGG AACCTCAGAG TCCAGATCTG AACGATGCCG 420
 TGTCCAGTTT GCGAAGTCCT ATTCCCCTCC TCCTGTCGTG TGCCTTTGTT CAGGTGGGGA 480
 25 TGTATTTTCAT GTAGAAGGTG GAAGAAGGCT GCTATGACTC TTTGGATGGG AGTCTGGCAA 540
 GAGGAAATYG GAAGATAAAA TAAATAATAA GTGAAATAAA AAAAAAAAAA AAAAATCGA 600
 30 GGGGGGGCCC GGTACCCAAT 620

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

45 ACAAGGTGTG TGTAAAGTTT ATGTTTGTA ACTGAATTCT ATCTTAAATC CAAAAGAAG 60
 TCGGGAGTAA TTCATTTTGT TAGCATAAAG ATCCCTAAGT TTTATTTTGA AATATCTGAT 120
 TTTTACACGT TAAAAAATAA CAGGGCATCG AGAGGATTCC TAGGTGACAT CCAGACTCCT 180
 50 TTAGCTTTGT GTGTGTGGCA CCGGTTAGTC TGCTTCTCTC TCCTTTCTTG CACTGCTTCA 240
 CACAGCCATG CCCTGCCAGC CCGGCAGGT GCCTTCCTGT CAATGTACAT TTGGGCTTCT 300
 55 GCTCATGCTG CCTCCCTCC CCTCCCCTGC CTCCCAACCC CGCCCCTTTT GTTCTCCAT 360
 GGAGTACTTC CATGGGTGTG CCTCCCCAG CCAAGCCATA ATAGGTGGTT TCCCCTTCGC 420
 TTCTGTAGCC CTTCAGACA TCCTCTGTTT AAGTAGGTG TTGACTTACT TCCCCTCTCC 480
 60

CCGSTAAAGC CATAAACTCC TTAAGGACAG GTAGCATTTCT TAGTATCTTC GTTCTTCTCA 540
ATGACCAGTA GACCATTAAA CATGTAGCAA ACAAATGTGA A 581

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(2) INFORMATION FOR SEQ ID NO: 75:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1843 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

AAACCCAACN CCCTCCGGTC CCCNAAAGAA AGCCCAGCCC AAATCCCAAG CCGGCAGTGA 60
20 GCCCGCGAAC AAGGCCCTCA AGACGCCAG NCGAACAAGC AGCCCCCAGG AGGCCCCGCA 120
AGAGAACTCC CTGGCGGCCC AAGCGGCGAG CTTCTGTGCG GCAGAACTCA GCCACCGAGA 180
GCGCAGACAG CATCGAGATT TATGTCCCGG AGNCCCAGAC CAGGCTCTGA GACCATGCAG 240
25 GAGGAAAGAA ACGATTTTAA ATCATTAAAA ACACAAAAC TAAGTGGGAA CGGAACAGAG 300
TTTTCTCAAC CTTTGCTATG GTTATTCTGT CTAGAGACCC TGAGCCAACT TTCAAATTGA 360
30 CGCATACAAG GGCTCACAAT TTGGCTTTTT TGGGTCCCTC CCAGCTTTAG GTTATGAAGA 420
TTTTACTCAC AAAAAAATC AACAAAAATC ACGAACTAG AAAACTTTTT TTTTCCTCTT 480
GCTGGCCGTG GTGGACTAGA TAGATGGACG TCGGCAACTC CCGGCCCAGC CTCCATACTG 540
35 CGGTCTTTTT ACTCGTTCTA TCTGATGAGA ACTCACAATA GCTTGTTTAC AAGATGACGA 600
CAGTCCAAGG GCAGCCTTGG GCACCTGCCA TGTCCCTCCT TTCCCAGCT ATCCCCGCTC 660
40 TGACCTTGAT TTTCATTCTT ATGTTTTTCT CTTTTCCTTT CAGAGCTCAC ACAGTGGTCA 720
CCATTGTGGC AAGCGGCTTT CTGGGTCTCA GCCCTCTCTG CGGTTGAGGG CCCAGAGGAC 780
AGAGAGATGG ACATGCGTCC CCTCCCTCCC CCCGCCAAGT GCTCACACAC AACCTCAGGC 840
45 GCACACACAC ACACGAGAT GGAGGCGCCT CACTGGGAGG TGCCCCGCCA GCCCTGGGCA 900
GTGTCAGGCA GGAATCACTC ACCGCTGAGC AGATGAGAGA AGTTTATGTC TTGGCGGGTG 960
50 GAAATGAGAC GAAGCCACAG TTATCACAAT CCAGACTCCT GCCCTTTTAT TTTCTCCAGC 1020
CCCTTCTTCC TTCAGCAAAA TCTAGGACTC CCGAGTGGCT TCCAGGGGGC CGTCAGTCCT 1080
CAGCCGCGCC TGTGTCCGGT GCCCGAGGGG CGGGCGGCGG TGTCTGTATG TATGTGTACA 1140
55 TATGCACATA GACCTTAGAG TGTATAGTTA ACAAACGCCC ATCTGCTCAC CCATGCCAC 1200
CCAGCGCCGC CGCCGCTGGC TCTCGGGGCA CCTGGCAGGA GCGGGGTGTG TGAATAGCAT 1260
60 ATATTTTAC ATGTACTATA TCTAGGTGTG TGTACAAGTG TGTGTAAAAA TATATACCTT 1320

GTGTGTAAAGC AGCCCTTTT TTTTTTGGTC TCCACCCCCC TCCCCCGCC CCGCACTCCT 1380
 AAGGGCCCAT CTGCCCAGCC TCTGAGTTTT CTGTCTATT TTTTTTTTAA CCCCAATTAT 1440
 5 CCTTCTCTCT CTCTGCCCC CGCATCCAC TCCCAGGGTG TCACGAGCCC TGAGCTGCAA 1500
 TGGCCCCGGC CTGCAGGGCG GGGTAGGGGA GGGCARGGCT SAGCCCCGAA GCCAGCTCAG 1560
 10 TACCTGAGGG GCTGCTCTAT GCTGTGTATG CGCTCTCTG GCATCCGAGA CATCCTCTTG 1620
 GTGGCGCTTG CTNGCAGGGG ACCCCCCCCC CGTCCCCAGG TGAACCAAGG GTCTGCTCCG 1680
 GGGCCCATTT CCAGCTTGGC CGCGTCTGT GACCTTGGGC AAGTCACTTG ACCTCTGTGT 1740
 15 GCCTCAACTT CCTCTCTGT AAAACGGGGA CAGTCCCTGC CCTCCCTAC CTCACAGGCA 1800
 TGTGTGAGA ATAAATGAGG TAACGTGTAA AAAAAAAAAA AAT 1843

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(2) INFORMATION FOR SEQ ID NO: 76:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TCGACCCACG CGTCCGGCTC CCGAGCCCT GCCAACCATG GTGAACCTGG GTCTGTCCCG 60
 35 GGTGGACGAC GCGTGGCTG CCAAGCACCC GGGACTCGGG GAGTATGCCG CATGCCAGTC 120
 ACACGCCCTC ATGAAGGGCG TTTTACCTT CGTCACAGGC ACCGGCATGG CCTTTGGCTT 180
 GCAGATGTC ATTCAGAGGA AGTTTCCATA CCTTTGCAG TGGAGCCTCC TAGTGGCCGT 240
 40 GGTTCAGGC TCTGTGGTCA GCTACGGGGT GACGAGAGTG GAGTCGGAGA AATGCAACAA 300
 CCTCTGGCTC TTCCTGGAGA CCGGGCAGCT CCCCAAAGAC AGGAGCACAG ATCAGAGAAG 360
 45 CTAGGAGAGC TCCAGCAGGG GCACAGAGGA TTGGGGGCAG GAGGAGTCTG GAACACAGCC 420
 TTCATGCCCC CTGACCCAG GCGACCCCT CCCACACCCT AGGGTACCCC AGTCGTATCC 480
 TCTGTCCGCA TGTGTGGCCA GGCCTGACAA ACACCTGCAG ATGGCTGCTG CCCCAACCTG 540
 50 GGACCTGCCC AGRAGGTGG AGCAGAAAGG GCTCTCCCTG GGGTGGTGT TCTCCTCTAG 600
 GGTATTGGGA TGCATGTTCT GCACTGCCAG CAGAGAGGGT GTGTCTGGG GCCACCACCT 660
 55 ATGGGACAG GGTGCAAGG GGCCTGTACA CTCTGTCAIT TCCTTTCTAG CCCCTGCATC 720
 TCCAACAAGT CCAAGGTGAC AGCTGGTGCT AGGGGCGTGG GGTAAATAAA TGGCTTATCC 780
 TTCTCTCCAC CCAAGTTTCC ACCTGACCAG GTGAAAAACA AATCAGAAGG GTAAGATGAT 840
 60

	GACAGGTCAC ATGAAACCTT TATTACCCTA CAGTTGATAT ATGAGGATCA CATGCAAGTT	900
	ACATACTGAG GATGTACAGG GAAGTTCCCA GCGCTGAACC CCAGAATTAG ACGTTTCGCAT	960
5	CAGCCCCGTA GGCCACGTGG ACACCACCAC AGCCTCTCTG TATGGGGGTC TGCTCTGTGA	1020
	GCACCTGGCA TGTAGGGGCA GAGCAAAAGG GGCCANGCTG GCCAGAGCCT GGCTGCTGGG	1080
10	NAGARGAGGG ACTTGTGGGS CACGCCACNT GCCTATCATT CCCAYTCAT CTATTAGCCA	1140
	AAGTCACTCC CCAGAGGCAG AGCTAGCCCG TTGTAGCCGT GTCTGTGTGG AGGGAAGCT	1200
	TCTGAGTGGG CAAGCCTACA CACAGCCCCG AGCCCCAAGA GGAGGAAGAG GTGGAGACCA	1260
15	GACGGAACCT CCACAAGTCC ATCATGGTTA CAGCTGGCTT CCCCCAGCA CCGAAGACCC	1320
	ACAGCATNGG CCCTGCTGCC CCCGACCAG CTCAGCTGCC ANGCTCACC TTGCCAGGAA	1380
20	TTGAAAGAAA GTTATTGAGT ACTAATTGGC CTCAGAGTNA CAGGAAGCTC AAGTTAAAGT	1440
	G	1441

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(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 910 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

35	GGCAGAGCTG GCCTTCGACT CGCTATGTCC ACTAACAATA TGTCCGACCC ACGGAGGCCG	60
	AACAAAGTGC TGAGGTGAGG ACCCCAGCGT CGTGGGCACG GGTTCGGGTT GTGGGTGTGG	120
40	ATCGGGGCCC TGGGAAGCGC CTGTCTATCC CGGGGGCAGG ACCTGAGCGC CCCTGACCTT	180
	CGAGCCTGTC GCAGGTACAA GCCCCGCCG AGCGAATGTA ACCCGGCCTT GGACGACCCG	240
45	ACGCCGGA CTACATGAACCT GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAAG	300
	CTGAAGTGGT GTGCTTGGGT CGCTGTCTAC TGCTCCTTCA TCAGCTTTGC CAACTCTCGG	360
	AGCTCGGAGG ACACGAAGCA AATGATGAGT AGCTTCATGT GAGACTTGCC CTACAGAACA	420
50	AGTGACTCTT GAGTAAGGGG TGGGGGGACC CCAGCCTGGC CATCCTAGAC TGACACCTCT	480
	CTCCTGTCTT CATGCTGTCC ATCTCTGCCG TGGTGATGTC CTATCTGCAG AATCCTCAGC	540
55	CCATGACGCC CCCATGGTGA TACCAGCCTA GAAGGGTCAC ATTTTGGACC CTGTCTATCC	600
	ACTAGGCCTG GGCTTTGGCT GCTAAACCTG CTGCCCTCAG CTGCCATCCT GGACTTCCCT	660
	GAATGAGGCC GTCTCGGTGC CCCCAGCTGG ATAGAGGGAA CCTGGCCCTT TCCTAGGGAA	720
60	CACCCTAGGC TTACCCCTCC TGCTCCCTT CCCCTGCCTG CTGCTGGGGG AGATGCTGTC	780

	CATGTTTCTA GGGGTATTCA TTTCCTTTCT CGTTGAAACC TGTTGTTAAT AAAGTTTTC	840
5	ACTCTGAAAA AAAAAAAAAA AAAAAAAC TYGRGGGGG GCCCGAACC CAATTCSCCG	900
	GATAGTGAGT	910
10	(2) INFORMATION FOR SEQ ID NO: 78:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 2776 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:	
	TCGACCCACG CGTCCGGGCG GGCAGTGATG GCGGCTGGTG ATGGGGACGT GAAGCTAGGC	60
	ACCCCTGGGA GTGGCAGCGA GAGCAGCAAC GACGGCGGCA GCGAGAGTCC AGGCGACGCG	120
25	GGAGCGGCAG CGRAAGGGG AGGCTGGGCG GCGGCGGCGT TGGCGCTTCT GACGGGGGGC	180
	GGGGAAATGC TGCTGAACGT GGCCTGGTG GCTCTGGTGC TGCTGGGGGC CTACCGGCTG	240
30	TGGTGCGCT GGGGCGGCG GGGTCTGGG GCCGGGGCCG GGGCGGGCGA GGAGAGCCCC	300
	GCCACCTCTC TGCCTCGCAT GAAGAAGCGG GACTTCAGCT TGGAGCAGCT GCGCCAGTAC	360
	GACGGCTCCC GCAACCCGCG CATCCTGCTC GCGGTCAATG GGAAAGTCTT CGACGTGACC	420
35	AAAGGAGCA AGTTCTACGG CCCGGCGGGT CCATATGGAA TATTTGCTGG TAGGGATGCC	480
	TCCAGAGGAC TGGCCACATT TTGCCTAGAT AAAGATGCAC TTAGAGATGA ATATGATGAT	540
40	CTCTCAGATT TGAATGCAGT ACAAATGGAG AGTGTTGAG AATGGGAAAT GCAGTTTAAA	600
	GAAAAATATG ATTATGTAGG CAGACTCCTA AAACCAGGAG AAGAACCATC AGAATATACA	660
	GATGAAGAAG ATACCAAGGA TCACAATAAA CAGGATTGAA CTTTGTAAAC AACCAAAGTC	720
45	AGGGGCCTTC AGAACTGCAA TTCTTACTCC CTTTCACAGA CTGTCCGGAG TCTTTGGGTT	780
	TGATTACCT GCTGCGAAAA ACATTCAACA AATTGTGTAC AAGATAAATT AATCTCACTA	840
50	TGAAGATTTG AATAACTAGA CATTATTTAT GCTGCCAAAC TCATTTGTTG CAGTTGTTTG	900
	TAATGTCTAG TGGGCTTCA TCATCTGAA AAGAAGGAGA CAGGGATTTT TTAAAGAGC	960
	AAGAAAGTCA CAATATTACT TCTTCCTTC CTTTTTCCT TCTTTCCTT CTTCTTTCTC	1020
55	TTTCTTTCTT TTTAAATAT ATTGAAGACA ACCAGATATG TATTTGCTAC TCAAGTGAC	1080
	AGATCTCCTC AAGAAACATC AAGGGACTCC TGTGTCACAT ACTGTGTTTT TATTTTAACA	1140
60	TGGGTGAGGG AGGCGACCTG ATCAGGGGAG GTGGGGGTAC ACATCAATTT GAGTTGTTCA	1200

	GGCTACTGAA ACATTAAAAAT GTGAATTCCTT AAACCTTTCTT TTTTGGCTTT GTCAGGGAAA	1260
	AGAAAAATAT CTTTATAAAG AAATCTTTGG AAATTAGGAG AAGGAATTTC AGGTGGGTTT	1320
5	AAGTCAGAGC TAGTTCCCCA ACAGAAAGAT CATTTGAAAC CAGTTTTTAT CCCTTCTCTT	1380
	TCCTTCCCTT TCCCTAAATC AAATCAATAT TAATTGTGCC TTATTTCACT TAACATAGAC	1440
10	TTGAATTATT TTTAGGGAAA GCCCCTATAA TGAATTCAGA AATCACTACA AGCAGCATTA	1500
	AGACTGAAGT TGGAAATATC TGTTGACCAT AAAACCTTGA TATCATTCTG TGTATATAGA	1560
	ATGTAAAAGG AATATTACAG TGTAACTGC CATATATGTA ATATACACAA ACTCAATTAG	1620
15	CATTGTAATG GCCAAATGCA TTCCCCCATG CTTTCTGTG TTCAAAAAA TTGAAAAACA	1680
	AATCAACTCT TATCCCCAAC AGCTGCCTAA TTTTAGGAGT CTGACCCTCC ACATCTCACT	1740
20	GGTGTGGGTG CATGGGGCTG TGGAGTGGGT GTCAGTATGG ATGTGTCTGA ATGTGTGAGG	1800
	CCTTGGAAGG GACTCTTTCT GCAGATACTG TAAATACAAG TACCATTTTA ATAAAGCATG	1860
	TACAATAAAC CAAAATAAGC TTGAGTTGGA CTTTATATAC AGAACTGTAA GCCAGTGCAT	1920
25	TATGATACAG TTGTAAGATT GTGCATTGA TTCAAGATAA GGAAAAATCT TGGAAATGAA	1980
	AAGCAGGCAC KGGTTAACCA AGTTGTACAC ATTGTACCAC ATTCAGCATA ACTTTAGGAA	2040
30	GAAATTCAC TTTGTGAACA TTCTCCAGAA ATCCAAGATT ATTCAGGTAA GAATTGGTAT	2100
	ATTAAATGTA CATCTTTTTA CTTTCTATTT TGATGCCAAC TGATTATACT AGACAATTAG	2160
	CACTCCAGGT GGTATTGAA CACAAAACAG TAAAAGAATA TTGCACTGAT AGATACTAAA	2220
35	TTATTATTTT ATTAGGTTGA AAAAGCCCTT ACTAAAAGCC CCTCATATAT CAATTACTTT	2280
	ATTTCAATTAT GACTACTTAG GTTCCGGGCT GGGGACAAGT TCACTTAAAA AGGCAATGTT	2340
40	ATTTAACAGG TCACCAGTTA AGACTTCTGC TTTGTAGATA CATGCAGAAG CCATCAAACA	2400
	AGGGGGRGCT TTTAACTGCA ACAATAAGCT AAAGTATGTA AAATACTACA TTCTATTGAG	2460
	TCTTGGAGTG TTTGTAGAA AGTTATCTTC AGCCAAATCT TTGCTGAAGA CTGGTTGTGG	2520
45	AGTGTGGTA AATGCTTTGT GTTTTATGT AAAATATTTT CTAACAAAA AATGTTAAAA	2580
	GTACATGTCC TCTGTAGTAA ACTGATATCT ATATATATGA ATCATTCAG CCTAAAGTCT	2640
50	AGTAATAAAC TGTACTTGTG AATAGAGAAA CCCTAAATAT TCATGCAGWA AAAATTATGC	2700
	GGTCTGTAA GAAAAATGAG TAATTTGTGT TTTGGACTTG AAATAAACAG TGTCTGTAG	2760
	ATAATTCCTC AACTTC	2776
55		

(2) INFORMATION FOR SEQ ID NO: 79:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

	COGCTGCTGA TAACTATGGC ATCCCCCGGG CCTGCAGGAA TTCGGCACGG AGCTACGGCG	60
10	COGCTGGCT CCTGCTGCA CCTGCAGGCT CGTCGCGGGT GGAGCCCACC CAAGACATCA	120
	GCATCAGCGA CCAGCTGGGG GGCCAGGACG TGCCCCGTGTT CCGGAACCTG TCCCTGCTGG	180
15	TGGTGGGTGT CGGCGCCGTG TTCTCACTGC TATTCCACCT GGGCACCCGG GAGAGGCGCC	240
	GGCCGCATGC GGAGAGCCA GCGAGCACA CCCCCCTGTT GGGCCCTGCC ACGGCCCAGC	300
	CCTGCTGCT CTGGAAGCAC TGGCTCCGGG AGCSGGCTTT CTACCAGGTG GGCATACTGT	360
20	ACATGACCAC CAGGCTCATC GTGAACCTGT CCCAGACCTA CATGGCCATG TACCTCACCT	420
	ACTCGCTCCA CCTGCCAAG AAGTTCATCG CGACCATTC CCTGGTGATG TACCTCAGCG	480
25	GCTTCTGTG CTCCTTCCTC ATGAAGCCCA TCAACAAGTG CATTGGGAGG AACATGACCT	540
	ACTTCTCAGG CCTCCTGGTG ATCCTGGCCT TTGCCGCTG GGTGGCGCTG GCGGAGGGAC	600
	TGGGTGTGGC CGTGTACGA GCGGCTGTGC TGCTGGGTGC TGGCTGTGCC ACCATCCTCG	660
30	TCACCTCGCT GGCCATGACG GCGACCTCA TCGGTCCCA CACGAACAGC GGACTKTCGT	720
	GTACGGCTCC ATGAGCTTCT TGGATAAGGT GGCCAATGGG CTGGCAGTCA TGGCCATCCA	780
35	GAGCCTGCAC CCTTGCCCCC CAGAGCTCTG CTGCAGGGCC TGCCTGAGCT TTTACCACTG	840
	GGCGATGGTG GCTGTGACGG GCGGCGTGGG CGTGGCCGCT GCCCTGTGTC TCTGTAGCCT	900
	CCTGCTGTGG CCGACCCGCC TGCAGCGTG GGACCGTGAT GCCCGGCCCT GACTCCTGAC	960
40	AGCCTCCTGC ACCTGTGCAA GGAACCTGT GGGACGCACG AGGATGCCCC CCARGGCCTT	1020
	GGGAAAAGC CCCCCTGCC CTTCACTCTT CTCTGGACCC CCACCCTCCA TCCTCACCCA	1080
45	GCTCCCGGG GTGGGTGCG GTGAGGGCAG CAGGGATGCC CGCCAGGGAC TTGCAAGGAC	1140
	CCCCTGGGTT TTGAGGTGT CCCATTCTCA ACTCTAATCC ATCCCAGCCC TCTGGAGGAT	1200
	TTGGGGTGCC CCTCTCGGCA GGAACAGGA AGTAGGAATC CCAGAAGGGT CTGGGGGAAC	1260
50	CCTAACCCCTG AGCTCAGTCC AGTTCACCCC TCACCTCCAG CCTGGGGGTC TCCAGACACT	1320
	GCCAGGGCCC CTTAGGACG GCTGGAGCCT GGAGGAGACA GCCACGGGGT GGTGGGCTGG	1380
55	GCCTGGACCC CACCGTGGTG GGCAGCAGG CTGCCCCGCA GCCTTGGTGG ACTCTGCTGG	1440
	CAGCAAATAA AGAGATGACG GCAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1500
	AAAAAAAAAA AAACCCACCG TCCGC	1525

60

(2) INFORMATION FOR SEQ ID NO: 80:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1563 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

	AATTCGGCAC GAGNCAGAAA CCTGCGGAAA ATGGTAGCGA TGGCGGCTGG GCCGAGTGGG	60
15	TGTCTGGTGC CGCGGTTTGG GCTACGGTTG TTGTTGGCGA CTGTGCTTCA AGCGGTGTCT	120
	GCTTTTGGGG CAGAGTTTTC ATCGGAGGCA TGCAGAGAGT TAGGCTTTTC TAGCAACTTG	180
20	CTTTGCAGCT CTTGTGATCT TCTCGGACAG TTCAACCTGC TTCAGCTGGA TCCTGATTGC	240
	AGAGGATGCT GTCAGGAGGA AGCACAATTT GAAACCAAAA AGCTGTATGC AGGAGCTATT	300
	CTTGAAGTTT GTGGATGAAA ATTGGGAAGG TTCCCTCAAG TCCAAGCTTT TGTTAGGAGT	360
25	GATAAACCCA AACTGTTTCTAG AGGACTGCAA ATCAAGTATG TCCGTGGTTC AGACCCCTGTA	420
	TTAAAGCTTT TGGACGACAA TGGGAACATT GCTGAAGAAC TGAGCATTTCT CAAATGGAAC	480
30	ACAGACAGTG TAGAAGAATT CCTGAGTGAA AAGTTGGAAC GCATATAAAT CTTGCTTAAA	540
	TTTTGTCTTA TCCTTTTGTG ACCTTATCAA ATGAAATATT ACAGCACCTA GAAAATAATT	600
	TAGTTTGTCT TGCTTCCATT GATCAGTCTT TTACTTGAGG CATTAATATAT CTAATTAAAT	660
35	CGTGAAATGG CAGTATAGTC CATGATATCT AAGGAGTTGG CAAGCTTAAC AAAACCCATT	720
	TTTTATAAAT GTCCATCCTC CTGCATTTGT TGATACCACT AACAAAATGC TTTGTAACAG	780
40	ACTTGGCGTT AATTATGCAA ATGATAGTTT GTGATAATG GTCCAGTTT ACGAACAACA	840
	GATTCTCTAA TTAGAGAGGT TAACAAGACA GATGATTACT ATGCCTCATG TGCTGTGTGC	900
	TCTTTGAAAG GAATGACAGC AGACTACAAA GCAAATAAGA TATACTGAGC CTCAACAGAT	960
45	TGCCCTGCTC TCAGAGTCTC TCCTATTTTT GTATTACCCA GCTTCTTTT TAATACAAAT	1020
	GTTATTTATA GTTACAATG AATGCACTGC ATAAAACTT TGTAGCTTCA TTATTGTAAA	1080
50	ACATATTCAA GATCCTACAG TAAGAGTGAA ACATTCACAA AGATTTCGCT TAATGAAGAC	1140
	TACACAGAAA ACCTTTCTAG GGATTTGTGT GGATCAGATA CATACTGGC AAATTTTGA	1200
	GTTTTACATT CTTACAGAAA AGTCCATTTA AAAGTGATCA TTTGTAAGAC CAAAATATAA	1260
55	ATAAAAAGTT TCAAAAATCT ATCTGAATTT GGAATCTTC TGGTTTGTTC TTTCATGTTT	1320
	AAAAATGATG TTTTCAATG CATTTTTC ATGTAAGCCC TTTTTCAGC CAAAATGTAA	1380
60	AAATGGCTGT AATATTTAAA ACTTATAACA TCTTATTGTT GGTAATAGTG CTTTATATTT	1440

GTCTGATTTT ATTTTTCAAA GTTTTTTCAT TTATGAACAC ATTTTCATG GTATATTATT 1500
 TAAGGAATAT CTCTTGATAT AGAATTTTTA TATTA AAAAT GATTTTCTT TGCTTAAAAA 1560
 5 AAA 1563

10 (2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

20 TGCACGCTGG CCATGTGGGN GTTGGGCCAC TGCACCCCC GCGCTGCAC GGGCCGCAAG 60
 TTGGCCCGCC TGGGGCTGGT GCGCTGCTG CGCTGGGCC ACAGATTGG CGGTCTGGTG 120
 CTGAGCCCCG TGGGCAAGCA GTACGCGTCC CCCGCAGACA GACAGCTGGT GGCGCAGTCT 180
 25 GGGGTGCGCC TCATCGACTG CTCCTGGGCC AGGCTGGACG AGACACCGTT TGGGAAGATG 240
 CGAGGGAGCC ACTTGCCTCT GTTGCCCTAC CTGGTGGCCG CCAACCCCGT GAACTATGGC 300
 30 CGGCCCTACA GACTTTCTCT CGTGAAGCG TTTGCTGCCA CCTTCTGCAT CGTAGGCTTT 360
 CCAGACCTTG CTGTCATTTT GCTGCGGAAG TTAAATGGG GCAAGGGCTT CTTGGACCTG 420
 AACC GCCAGC TCCTGGACAA GTACCGGCC TCGGCAGCC CGGAGGAGT GCTGCAGGCG 480
 35 GAGCAGGAGT TCCTGGCCAA TGCCAAGGAG AGCCCCCAGG AGGAGGAGAT CGATCCCTTC 540
 GATGTGGATT CAGGGAGAGA GTTGGAAAC CCCAACAGGC CTGTGGCCAG CACCCGGCTG 600
 40 CCCTCGGACA CTGATGACAG TGATGCGTCT GAGGACCCAG GGCCTKCGC CGAGCGCGGA 660
 GGAGCCAGCA GCAGCTGCTG TGAAGAGGAG CAGACGAGG GACGGGGGCG TGAGGCCAGG 720
 GCCCCGGCTG AGGTTTGGAA AGGAATCAAG AAACGGCAGA GAGACTGAGG GTTGCAGACA 780
 45 CATATATTTT TGAGGCTGGG TGACGAGAAA ATCTAGAGAC ATGAGGGACA TAAATGGGCC 840
 TGGCAGCCTC GGCTCTTTGC GGCTGCTGGC AGGACTGAGC TGTCCGGGTT CTCCCCACAC 900
 50 TTCCAGCACA GCTGTGCTCT GTGTCCTGCC TCGGCGCTCT CGCAAATGAA GCTGCAGGCC 960
 AAGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAG GGGGGGGGGC 1020

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(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TCGACCCACG CGTCCGGGCC GCCGTAGCGC GTCTTGGGTC TCCCGGCTGC CGCTGCTGCC 60
GCCGCCGCCT CGGGTCGTGG AGCCAGGAGC GACGTCACCG CCATGGCAGG CATCAAAGCT 120
10 TTGATTAGTT TGTCTTTTGG AGGAGCAATC GGA CTGATGT TTTTTRATGCT TGGATGTGCC 180
CTTCCAATAT ACAACAAATA CTGGCCCCCTC TTTGTTCTAT TTTTTTACAT CCTTTCACCT 240
15 ATTCCATACT GCATAGCAAG AAGATTAGTG GATGATACAG ATGCTATGAG TAACGCTTGT 300
AAGGAACTTG CCATCTTTCT TACAACGGGC ATTGTCGTGT CAGCTTTTGG ACTCCCTATT 360
GTATTTGCCA GAGCACATCT GATTGAGTGG GGAGCTTGTG CACTTGTCTT CACAGGAAAC 420
20 ACAGTCATCT TTGCAACTAT ACTAGGCTTT TTCTTGGTCT TTGGAAGCAA TGACGACTTC 480
AGCTGGCAGC AGTGGTGAAA AGAAATTACT GAACTATTGT CAAATGGACT TCCTGTCATT 540
25 TGTGTGGCCAT TCACGCACAC AGGAGATGGG GCAGTTAATG CTGAATGGTA TAGCAAGCCT 600
CTTGGGGGTA TTTTAGGTGC TCCCTTCTCA CTTTATTGT AAGCATACTA TTTTCACAGA 660
GACTTGCTGA AGGATTAAAA GGATTTTCTC TTTTGGAAAA AAAAAAAAAA AAAAACYCGA 720
30 GGGGGGGCCC GTWCCCATTC SCCCATATG AATTCNTTT TTACAATCCC 770

35

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

GAATTCGGCA CGAGCATAGT GTTAACCACT AGAATTCAC TCCCTTCCTA TCCAAAAATG 60
ACACTACTGA TCATTTTTCT TCCTTTTST TTTACAACAT TMACAAATTC AGGTGGCTCT 120
50 TTCCCACTAC GGTAGGCTGA TTCGTATGGA TGCACCACGG TTGGTGACTC CCCCCACCCC 180
ACAGAGTTTC TGGCGTTCAT TCGGTGAAC CCAAGGCCAG CAAGGGCTGA CTGGGAACAA 240
ACCGAACACT AGGCCGTGAA CCAATCGTCT CTCCGTGCCC GGGAGCGAMC CCGGGGGCCT 300
55 TTCCTCTCC CAAGGACTCC ANGGGGGGC CGGGTACCCA ATTCCGCCCC TATAGTGAAT 360
CCGTNATTAC AATTCACANT GGGCCGTCCN TTTTACAAA CGTTCCGTTG AACTGGGAAA 420
60 AACCCCTTGG CGGTTTACCC CAACTTTAAT CCGCCTTTC AAGCACATCC CCCCCCTTTT 480

C

481

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(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 644 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GCTGGGATAG AGCATGAAAG GAGAACTGCT CCCTTTTCTG TTTCTCACAG TTTGGTTATG 60
 GCTTTATAAA CTTKTATTTG GTGAAAGCCC CAGATACCCA AATGTCATTG GCAAAACTTA 120
 20 TTTTTTTTTT TGGACAGATC AGATTTCTAG AGAGAGCAGA TTTCTAGAGA GATTAGCATT 180
 CATAGTAAGT GAAAATGTGC TAATTTTTTT AATCCATGCT ATTACTGGGC AGTAGGTCTA 240
 25 ATTTTTTTTG ACAAAAAATA GATCTATTTT CCTTATATAT TGATTTAGAA TCTTAAGTTA 300
 GAATTTTATA GAAGAAATGT CTGAGCAGTT CTATGTATGG AGGAGCAATT CAGCTTTTCA 360
 GCAGCAACTT TATCTTTTGC CACTAGAGGG AGATCTGTGG TTGCTTTCTC CTTTGGAGAA 420
 30 TAGCTGCTTT GCTTTTATTT TTAATTTCTA AGGTTGGAAT AGAACTTATT CTCAAAATTC 480
 CTTTAGTGTT ATTAAATATT TTCATTTATT AGTCAAAGGT AAGTTAATTA AGCTTGTTTA 540
 35 ATGATGCCAA TCTTAGCTT TTCTGTAATC TTCAATTTT AATAAATGTG AGTTAGATAC 600
 TAAGTGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 644

40

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GGCAGAGTG CGCAGCGTG GGGCTCTCTC CTGTCTAGTC GGCGCCGCGT GCGGGCTGGT 60
 GGCTCTGTGG CAGCGGCGGC GGCAGGACTC CGGCACTATG AGCGGCTTCA GCACCGAGGA 120
 55 GCGCGCCGCG CCNTTCTCCC TGGAGTACCG AGTCTTCTC AAAAAAGAGA AAGGACAATA 180
 TATATCTCCA TTTCATGATA TTCCAATTTA TGCAGATAAG GATGTGTTTC ACATGGTAGT 240
 60 TGAAGTACCA CGCTGGTCTA ATGCAAAAAT GGAGATTGCT ACAAAGGACC CTTTAAACCC 300

	TATTAAACAA GATGTGAAAA AAGGAAAAC TCGCTATGTT GCGAATTTGT TCCCGTATAA	360
	AGGATATATC TGGAACTATG GTGCCATCCC TCAGACTTGG GAAGACCCAG GGCACAATGA	420
5	TAAACATACT GGCTGTTGTG GTGACAATGA CCCAATTGAT GTGTGTGAAA TTGGAAGCAA	480
	GGTATGTGCA AGAGGTGAAA TAATTGGCGT GAAAGTTCTA GGCATATTGG CTATGATTGA	540
10	CGAAGGGGAA ACCGACTGGA AAGTCATTGC CATTAAATGTG GATGATCCTG ATGCAGCCAA	600
	TTATAATGAT ATCAATGATG TCAAACGGCT GAAACCTGGC TACTTAGAAG CTA CTGTTGGA	660
	CTGGTTTAGA AGGTATAAGG TTCCTGATGG AAAACCAGAA AATGAGTTTG CGTTTAATGC	720
15	AGAATTTAAA GATAAGGACT TTGCCATTGA TATTATTAAA AGCACTCATG ACCATTGGAA	780
	AGCATTAGTG ACTAAGAAAA CGAATGGAAA AGGAATCAGT TGCATGAATA CAACTTTGTC	840
20	TGAGAGCCCC TTCAAGTGTG ATCCTGATGC TGCCAGAGCC ATTGTGGATG CTTTACCACC	900
	ACCCGTGTGAA TCTGCCTGCA CAGTACCAAC AGACGTGGAT AAGTGGTTCC ATCACCAGAA	960
	AAACTAATGA GATTTCCTCG GAATACAAGC TGATATTGCT ACATCGTGT CATCTGGATG	1020
25	TATTAGAAGT AAAAGTAGTA GCTTTTCAAA GCTTTAAATT TGTAGAACTC ATCTAACTAA	1080
	AGTAAATTCT GCTGTGACTA ATCCAATATA CTCAGAATGT TATCCATCTA AAGCATTTTT	1140
30	CATATCTCAA CTAAGATAAC TTTTAGCACA TGCTTAAATA TCAAAGCAGT TGTCATTGCG	1200
	AAGTCACTTG TGAATAGATG TGCAAGGGGA GCACATATTG GATGTATATG TTACCATATG	1260
	TTAGGAAATA AAATTATTTT GCTGAAAAAA AAAAAAAAAA AACCNCGGGG GGGGCCCCGG	1320
35	TCCCCATTG GCCCTTTGGG GGGNGGTTTT A	1351

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(2) INFORMATION FOR SEQ ID NO: 86:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

	CTCTTGCTAC CTTCCCGGCG CAGAGAACCC CGGCTGCTCA GCGCGCTCCG GGGTCATGGA	60
	GATCCCCGGG AGCCTGTGCA AGAAAGTCAA GCTGAGCAAT AACGCGCAGA ACTGGGGAAT	120
55	GCAGAGAGCA ACCAATGTCA CCTACCAAGC CCATCATGTC AGCAGGAACA AGAGAGGTCA	180
	GGTGGTGGGG ACCAGAGGTG GCTTTCGTGG TTGCACAGTT TGGCTAACAG GCTTGTCTGG	240
60	AGCGGGAAAG ACTACTGTGA GCATGGCCTT GGAGGAGTAC CTGGTTTGTC ATGGTATTCC	300

	ATGCTACACT CTGGATGGTG ACAATATTCG TCAAGGTCTC AATAAAAATC TTGGCTTTAG	360
	TCCTGAAGAC AGAGAAGAGA ATGTTGACG CATCGCAGAA GTTGCTAAAC TGTTTGACAGA	420
5	TGCTGGCTTA GTGTGCATCA CAAGTTTCAT ATCACCTTAC ACTCAGGATC GCAACAATGC	480
	AAGGCCAAATT CATGAAGGTG CAAGTTTACC GTTTTITGAA GTATTTGPTG ATGCTCCTCT	540
10	GCATGTTTGT GAACAGAGGG ATGTCAAAGG ACTCTACAAA AAAGCCCGGG CAGGAGAAAT	600
	TAAAGGTTTC ACTGGGATCG ATTCTGAATA TGAAAAGCCA GAGGCCCTG AGTTGGTGCT	660
	GAAAACAGAC TCCTGTGATG TAAATGACTG TGTCCAGCAA GTTGTGGAAC TTCTACAGGA	720
15	ACGGGATATT GTACCTGTGG ATGCATCTTA TGAAGTAAAA GAACTATATG TGCCAGAAAA	780
	TAAACTTCAT TTGGCAAAAA CAGATGCGGA AACATTACCA GCACTGAAAA TTAATAAAGT	840
20	GGATATGCAG TGGGTGCAGG TTTTGGCAGA AGGTTGGGCA ACCCCATTGA ATGGCTTTAT	900
	GAGAGAGAGG GAGTACTTGC AGTGCCTTCA TTTTGATTGT CTCTGGATG GAGGTGTCAT	960
	TAACPTGTCA GTACCTATAG TTCTGACTGC GACTCATGAA GATAAAGAGA GGCTGGACGG	1020
25	CTGTACAGCA TTTGCTCTGA TGTATGAGGG CCGCCGTGTG GCCATTCTTC GCAATCCAGA	1080
	GTTTTTITGAG CACAGGAAAG AGGAGCGCTG TGCCAGACAG TGGGGAACGA CATGCAAGAA	1140
30	CCACCCCTAT ATTAAGATGG TGATGGAACA AGGAGATTGG CTGATTGGAG GAGATCTTCA	1200
	AGTCTTGGAT CGAGTTTATT GGAATGATGG TCTTGATCAG TATCGTCTTA CTCCTACTGA	1260
	GCTAAAGCAG AAATTTAAAG ATATGAATGC TGATGCTGTC TTTGCATTTC AACTACGCAA	1320
35	CCCAGTGCAC AATGGACATG CCCTGTTAAT GCAGGATACC CATAAGCAAC TTCTAGAGAG	1380
	GGGCTACCGG CGCCCTGTCC TCCTCCTCCA CCCTCTGGGT GGCTGGACAA AGGATGACGA	1440
40	TGTTCCTTTG ATGTGGCGTA TGAAGCAGCA TGCTGCAGTG TTGGAGGAAG GAGTTCTGAA	1500
	TCCTGAGACG ACAGTGGTGG CCATCTTCCC ATCTCCCATG ATGTATGCTG GACCAACTGA	1560
	GGTCCAGTGG CATTCAGAG CACGGATGGT TGCAGGAGCC AACTTTTACA TTGTTGGACG	1620
45	AGACCTGCT GGCATGCCTC ATCCAGAAAC AGGGAAGGAT CTTTATGAGC CAAGTCATGG	1680
	TGCCAAAGTG CTGACGATGG CCCCTGGTTT AATCACTTTG GAAATAGTTC CCTTTCGAGT	1740
50	TGCAGCTTAC AACAAGAAAA AGAAGCGTAT GGACTIONAT GACTCTGAAC ACCATGAAGA	1800
	CTTTGAATTT ATTTTCAGGAA CACGAATGCG CAAACTTGCT CGAGAAGGCC AGAAACCACC	1860
	TGAAGGTTTC ATGGCTCCCA AGGCTTGGAC CGTGCTGACA GAATACTACA AATCCTTGGA	1920
55	GAAAGCTTAG GCTGTTAACC CAGTCACTCC ACCTTTGACA CATTACTAGT AACAAGAGGG	1980
	GACCACATAG TCTCTGTTGG CATTTCTTTG TGGTGTCTGT CTGGACATGC TTCTAAAAA	2040
60	CAGACCATTT TCCTTAACTT GCATCAGTTT TGGTCTGCCT TATGAGTTCT GTTTTGAACA	2100

AGTGTAAACAC ACTGATGGTT TTAATGTATC TTTTCCACTT ATTATAGTTA TATTCCTACA 2160
 ATACAATTTT AAAATGTGCT TTTTATATTA TATTTATGCT TCTGTGTCAT GATTTTMTCA 2220
 5 AGCTGTTATA TTAGTTGTAA CCAGTAGTAT TCACATTAAA TCTTGCTTTT TTTCCCTTA 2280
 AAAAAAGAAA AAAATTACCA AACAATAAAC TTGGCTAGAC CTGTTTGTGA GGATTTTACA 2340
 AGACCTTTGT AGCGATTAGA TTTTMTTCT ACATTGAAAA TAGAACTGC TTCCTTTCTT 2400
 10 CTTTCCAGTC AGCTATTGGT CTTTCCAGCT GTTATAATCT AAAGTATTCT TATGATCTGT 2460
 GTAAGCTCTG AATGAACTTC TTTACTCAAT AAAATTAATT TTTTGGCTTC TTAACAAAAA 2520
 15 AAAAAA 2527

20 (2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2566 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

30 CCCAAGAATT CGGCACGAGC GNGGCAWAAK TGGGATTTCT GAAACCTGTA GGCCCAAGC 60
 CCATCAACTT GCCCAAAGAA GATTCCAAAC CTACATTTCC CTGGCCTSCT GGAAACAAGC 120
 CATCTCTTCA CAGTGTAAC CAAGACCATG ACTTAAAGCC ACTAGGCCGA AATCTGGGCC 180
 35 TACTCTCCA ACCTCAGAAA ATGAACAGAA GCAAGCKTTT CCCAAATTGA CTGGGGTTAA 240
 AGGGAAATTT ATGTCAGCAT CACAAGATCT TGAACCCAAG CCCCTCTTCC CCAAACCCGC 300
 40 CTTTGGCCAG AAGCCGCCCC TAAGTACCGA GAACTCCCAT GAAGACGAAA GCCCATGAA 360
 GAATGTGCT TCATCAAAAG GGTCCCAGC TCCCCTGGGA GTCAGGTCCA AAAGCGGCC 420
 TTTAAACCA GCAAGGAAG ACTCAGAAA TAAAGACCAT GCAGGGGAGA TTTCAAGTTT 480
 45 GCCCTTTCTT GGAGTGGTTT TGAAACCTGC TGCAGCAGG GGAGGCCAG GTCTCTCAA 540
 AAATGGTGAA GAAAAAAGG AAGATAGGAA GATAGATGCT GCTAAGAACA CCTTCCAGAG 600
 50 CAAATAAAT CAGGAAGAGT TGGCCTCAGG GACTCCTCCT GCCAGGTTC CTAAGCCCC 660
 TTCTAAGCTG ACAGTGGGG GGCCATGGGG CCAAAGTCAG GAAAAGGAAA AGGGAGACAA 720
 GAATTCAGCC ACCCGGAAAC AGAAGCCATT GCCTCCCTTG TTTACCTTGG GTCCACCTCC 780
 55 ACCAAAACCC AACAGACCAC CAAATGTTGA CCTGACGAAA TTCCACAAAA CCTCTCTGG 840
 AAACAGTACT AGCAAAGGCC AGACGTCTTA CTCAACAACT TCCCTGCCAC CACCTCCACC 900
 60 ATCCCATCCG GCCAGCCAAC CACCATTGCC AGCATCTCAC CCATCACAAC CACCAGTCCC 960

	AAGCCTACCT CCCAGAAACA TTAAACCTCC GTTTGACCTA AAAAGCCCTG TCAATGAAGA	1020
5	CAATCAAGAT GGTGTCACGC ACTCTGATGG TGCTGGAAT CTAGATGAGG AACAGACAG	1080
	TGAAGGAGAA ACATATGAAG ACATAGAAGC ATCCAAAGAA AGAGAGAAGA AAAGGGAAAA	1140
	GGAAGAAAAG AAGAGGTTAG AGCTGGAGAA AAAGGAACAG AAAGAGAAAG AAAAGAAAGA	1200
10	ACAAGAAATA AAGAAGAAAT TTAAACTAAC AGGCCCTATT CAAGTCATCC ATCTTGCAAA	1260
	AGCTTGTTGT GATGTCAAAG GAGGAAAGAA TGAAGTGGC TTCAAGCAAG GAGAGCAAAT	1320
15	TGAAATCATC CGCATCACAG ACAACCCAGA AGGAAATGG TTGGGCAGAA CAGCAAGGGG	1380
	TTCATATGGC TATATTAAAA CAACTGCTGT AGAGATTGAC TATGATTCTT TGAACTGAA	1440
	AAAAGACTCT CTGGTGCCC CTTCAAGACC TATTGAAGAT GACCAAGAAG TATATGATGA	1500
20	TGTTGCAGAG CAGGATGATA TTAGCAGCCA CAGTCAGAGT GGAAGTGGAG GGATATTCCC	1560
	TCCACCACCA GATGATGACA TTTATGATGG GATTGAAGAG GAAGATGCTG ATGATGGCTC	1620
25	CACACTACAG GTTCAAGAGA AGAGTAATAC GTGGTCCTGG GGGATTTTGA AGATGTTAAA	1680
	GGGAAAAGAT GACAGAAAGA AAAGTATACG AGAGAAACCT AAAGTCTCTG ACTCAGACAA	1740
	TAATGAAGGT TCATCTTTCC CTGCTCCTCC TAAACAATTG GACATGGGAG ATGAAGTTTA	1800
30	CGATGATGTG GATACCTCTG ATTTCCCTGT TTCATCAGCA GAGATGAGTC AAGGAACTAA	1860
	TGTTGGAAAA GCTAAGACAG AAGAAAAGGA CCTTAAGAAG CTAAAAAGC AGRAAAAARA	1920
35	ARAAAAGAC TTCAGGAAAA AATTTAAATA TGATGGTGAA ATTAGAGTCC TATATTCAAC	1980
	TAAAGTTACA ACTTCCATAA CTTCTAAAAA GTGGGAACC AGAGATCTAC AGGTAAAACC	2040
	TGGTGAATCT CTAGAAGTTA TACAAACCAC AGATGACACA AAAGTTCTCT GCAGAAATGA	2100
40	AGAAGGGAAA TATGGTTATG TCCTTCGGAG TTACCTAGCG GACAATGATG GAGAGATCTA	2160
	TGATGATATT GCTGATGGCT GCATCTATGA CAATGACTAG CACTCAACTT TGGTCATTCT	2220
45	GCTGTGTTCA TTAGGTGCCA ATGTGAAGTC TGGATTTTAA TTGGCATGTT ATTGGGTATC	2280
	AAGAAAATTA ATGCACAAAA CCACTTATTA TCATTTGTTA TGAAATCCCA ATTATCTTTA	2340
	CAAAGTGTIT AAAGTTTGAA CATAGAAAAT AATCTCTCTG CTTAATTGTT ATCTCAGAAG	2400
50	ACTACATTAG TGAGATGTAA GAATTATTAA ATATTCCATT TCCGCTTTGG CTACAATTAT	2460
	GAAGAAGTTG AAGGTACTTC TTTTAGACCA CCAGTAAATA ATCCTCCTTC AAAAAATAAA	2520
55	AATAAAAAAA AAAAAAAA ACTCGAGGGG GGGCCCGGTA CCCAAT	2566

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

10 GAATTCGGCA CGAGGCTTTC TGTGTCTCT GTGGCTGCTT TAGTGTGCCA CCAGGGGCAG 60
ACTTGGGTGG GTTGCAGCAG AGATGGCATG GCCCTCAAGG TCCAAGATGT TTACTCTCTT 120
GCCGGTCTCT TGTATCTCT GGTCTTTGTG GTTGCCACAG TTTTCTTGA TCCAGGAGTT 180
15 AAAGGCAGTC CTGAGGGATG ATGGCCTCAT CTCGCAGTT GCYTGAATG CTGAATTTCA 240
GACGTGCTAA AGGAGGGTTG CAGACATTGT GTGGWATGCA TTCAGACCCC AGATGTGGGT 300
GCAGGAAGGC AGGCATGGCA CAGCCAGGTA GAGACTGGTT TCCAGGCCCA AGCAGCCTTC 360
20 AGCAGCTGTG CGCCTTGTTT CTGATGTTGT TTGGGAGTAA GAATAATGTA GACATGGGGG 420
GTCATGARGC TCAATAAAAA CTTCAAGGAA ACCTCCCATG GCATGGTTGG GCGCAGTGAC 480
25 TCATGCCTGT AACCCAGCA CTGTGGAATG CCAAGGTGA AGGATCGCTT GAGGCCAAGA 540

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

40 TCGACCCACG CGTCCGGCGA GATCCCTACC GCAGTAGCCG CCTCTGCCGC CGCGGAGCTT 60
CCCGAACCTC TTCAGCCGCC CGGAGCCGCT CCCGGAGCCC GGCCGTAGAG GCTGCAATCG 120
CAGCCGGGAG CCCGAGCCC GCGCCCGAG CCCGCCGCC CCCTTCGAGG GCGCCCCAGG 180
45 CCGCGCCATG GTGAAGGTGA CGTTCAACTC CGCTCTGGCC CAGAAGGAGG CCAAGAAGGA 240
CGAGCCCAAG AGCGGCGAGG AGGCGCTCAT CATCCCCCC GACGCCGTCG CGGTGGACTG 300
50 CAAGGACCCA GATGATGTGG TACCAGTTGG CCAAAGAAGA GCCTGGTGTT GGTGCATGTG 360
CTTTGGACTA GCATTTATGC TTGCAGGTGT TATTCTAGGA GGAGCATACT TGTACAAATA 420
TTTTGCACCT CAACCAGATG ACGTGTACTA CTGTGGAATA AAGTACATCA AAGATGATGT 480
55 CATCTTAAAT GAGCCCTCTG CAGATGCCCC AGCTGCTCTC TACCAGACAA TTGAAGAAAA 540
TATTAAAATC TTGAAGAAG AAGAAGTTGA ATTTATCAGT GTGCCTGTCC CAGAGTTTGC 600
60 AGATAGTGAT CTGCCAACA TTGTCATGA CTTTAAACAAG AACTTACAG CCTATTTAGA 660

	TCTTAACCTG GATAAGTGCT ATGTGATCCC TCTGAACACT TCCATTGTTA TGCCACCCAG	720
5	AAACCTACTG GAGTTACTTA TTAACATCAA GGCTGGAACC TATTTGCCTC AGTCCTATCT	780
	GATTCAATGAG CACATGGTTA TTAATGATCG CATTGAAAAC ATTGATCACC TGGGTTTCTT	840
	TATTTATCGA CTGTGTCATG ACAAGGAAAC TTACAACTG CAACGCAGAG AAATATTAA	900
10	AGGTATTGAG AAACGTGAAG CCAGCAATTG TTTCCGAATT CGGCATTTTG AAAACAAATT	960
	TGCCGTGGAA ACTTTAATTT GTTCTTGAAC AGTCAAGAAA AACATTATTG AGGAAAATTA	1020
15	ATATCACAGC ATAACCCAC CCTTTACATT TTGTGCAGTG ATTAATTTTTT AAAGTCTTCT	1080
	TTTATGTAAG TAGCAACAG GGCTTTACTA TCTTTTCATC TCATTAATTC AATTAAAACC	1140
	ATTACCTTAA AATTTTTTTC TTTTGAAGTG TGGTGTCTTT TATATTTGAA TTAGTAACTG	1200
20	TATGAAGTCA TAGATAATAG TACATGTCAC CTTAGGTAGT AGGAAGAATT ACAATTTCTT	1260
	TAAATCATTT ATCTGGATTT TTATGTTTTA TTAGCATTTT CAAGAAGACG GATTATCTAG	1320
25	AGAATAATCA TATATATGCA TACGTAAAAA TGGACCACAG TGACTTATTT GTAGTTGTTA	1380
	GTGCCCCTGC TACCTAGTTT GTTAGTGCAAT TTGAGCACAC ATTTTAATTT TCCTCTAATT	1440
	AAAATGTGCA GTATTTTCAG TGTCAAATAT ATTTAACTAT TTAGAGAATG ATTTCCACCT	1500
30	TTATGTTTTA ATATCCTAGG CATCTGCTGT AATAATATTT TAGAAAAATG TTGGAATTTA	1560
	AGAAATAACT TGTGTTACTA ATTTGTATAA CCCATATCTG TGCAATGGAA TATAAATATC	1620
35	ACAAAGTTGT TTAACATGAC TGGTGTGTTG TTTTCCCGTA TAATAAAACC AAAGAATAGT	1680
	TTGGTTCTTC AAATCTTAAG AGAATCCACA TAAAAGAAGA AACTATTTTTT TAAAAATTCA	1740
	CTTCTATATA TACAATGAGT AAAATCACAG ATTTTTCCTT TAAATAAAAA TAAGTCATTT	1800
40	TAATAACTAA ACCAGATTCT TTGTGATACT ATTAANGTAA CATTTAGCCC CAAAAAATAA	1860
	AAA	1863

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(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

	GGCACAGCGG CACGAGGTGA GCTGAGCCGG TGGGTGAGCG GCGGCCACGG CATCCTGTGC	60
60	TGTGGGGGCT ACGAGGAAAG ATCTAATTAT CATGGACCTG CGACAGTTTC TTATGTGCCT	120

	GTCCCTGTGC ACAGCCTTTG CCTTGAGCAA ACCCACAGAA AAGAAGGACC GTGTACATCA	180
	TGAGCCTCAG CTCAGTGACA AGGTTACAAA TGATGCTCAG AGTITTTGATT ATGACCATGA	240
5	TGCCTTCTTG GGTGCTGAAG AAGCAAAGAC CTTTGATCAG CTGACACCAG AAGAGAGCAA	300
	GGAAAGGCTT GGAAAGATTG TAAGTAAAT AGATGGCGAC AAGGACGGGT TTGTCACTGT	360
	GGATGAGCTC AAAGACTGGA TTAAATTTGC ACAAAGCGC TGGATTTACG AGGATGTAGA	420
10	GCGACAGTGG AAGGGGCATG ACCTCAATGA GGACGGCCTC GTTTCCTGGG AGGAGTATAA	480
	AAATGCCACC TACGGCTACG TTTTAGATGA TCCAGATCCT GATGATGGAT TTAACATAA	540
15	ACAGATGATG GTTAGAGATG AGCGGAGGTT TAAATGGCA GACAAGGATG GAGACCTCAT	600
	TGCCACCAAG GAGGAGTTCA CAGCTTTCCT GCACCTGAG GAGTATGACT ACATGAAAGA	660
	TATAGTAGTA CAGGAAACAA TGAAGATAT AGATAAGAAT GCTGATGGTT TCATTGATCT	720
20	AGAAGAGTAT ATTGGTGACA TGTACAGCCA TGATGGGAAT ACTGATGAGC CAGAATGGGT	780
	AAAGACAGAG CGAGAGCAGT TTGTTGAGTT TCGGGATAAG AACCGTGATG GGAAGATGGA	840
25	CAAGGAAGAG ACCAAAGACT GGATCCTTCC CTCAGACTAT GATCATGCAG AGGCAGAAGC	900
	CAGGCACCTG GTCTATGAAT CAGACCAAAA CAAGGATGGC AAGCTTACCA AGGAGGAGAT	960
	CGTTGACAAG TATGACTTAT TTGTTGGCAG CCAGGCCACA GATTTTGGGG AGGCCTTAGT	1020
30	ACGGCATGAT GAGTTCCTGAG CTRCGGAGGA ACCCTCATTT CCTCAAAAGT AATTTATTTT	1080
	TACAGCTTCT GGTTCACAT GAAATTGTTT GCGCTACTGA GACTGTTACT ACAAACTTTT	1140
35	TAAGACATGA AAAGGCGTAA TGAAAACCAT CCCGTCCCA TTCCTCCTCC TCTCTGAGGG	1200
	ACTGGAGGGA AGCCGTGCTT CTGAGGAACA ACTCTAATTA GTACACTTGT GTTTGTAGAT	1260
	TTACACTTTG TATTATGTAT TAACATGGCG TGTATTATTT TGTATTTTC TCTGGTTGGG	1320
40	AGTATGATAT GAAGATCAA GATCCTCAAC TCACACATGT AGACAAACAT TAGCTCTTTA	1380
	CTCTTTCTCA ACCCCTTTTA TGATTTTAAT AATTCTCACT TAACTAATTT TGTAAGCCTG	1440
45	AGATCAATAA GAAATGTTCA GGAGAGAGGA AAGAAAAAA ATATATGCTC CACAATTTAT	1500
	ATTTAGAGAG AGAACACTTA GTCTTGCTG TCAAAAAGTC CAACATTTCA TAGGTAGTAG	1560
	GGGCCACATA TTACATTGAG TTGCTATAGG TCCAGCAACT GAACCTGCCA TTACCTGGGC	1620
50	AAGGAAAGAT CCCTTTGCTC TAGGAAAGCT TGGCCCAAAT TGATTTTCTT CTTTTTCCCC	1680
	CTGTAGGACT GACTGTTGGC TAATTTTGTC AAGCACAGCT GTGGTGGGAA GAGTTAGGGC	1740
55	CAGTGTCTTG AAAATCAATC AAGTAGTGAA TGTGATCTCT TTGCAGAGCT ATAGATAGAA	1800
	ACAGCTGGAA AACTAAAGGA AAAATACAAG TGTTTTCGGG GCATACATTT TTTTCTGGG	1860
60	TGTGCATCTG TTGAAATGCT CAAGACTTAA TTATTTGCCT TTTGAAATCA CTGTAAATGC	1920

	CCCCATCCGG TTCTCTTTCT TCCCAGGTGT GCCAAGGAAT TAATCTTGGT TTCACTACAA	1980
	TTAAAATTCA CTCCTTTCCA ATCATGTGTCAT TGAAAGTGCC TTAAACGAAA GAAATGGTCA	2040
5	CTGAATGGGA ATTCTCTTAA GAAACCCTGA GATTAAAAAA AGACTATTTG GATAACTTAT	2100
	AGGAAAGCCT AGAACCTCCC AGTAGAGTGG GGATTTTTTT CTCTTCCCT TTCTCTTTTG	2160
10	GACAATAGTT AAATTAGCAG TATTAGTTAT GAGTTTGGTT GCAGTGTCT TATCTTGTGG	2220
	GCTGATTTCC AAAAACCACA TGCTGCTGAA TTTACCAGGG ATCCTCATAC CTCACAATGC	2280
	AAACCACTTA CTACCAGGCC TTTTCTGTG TCCACTGGAG AGCTTGAGCT CACACTCAAA	2340
15	GATCAGAGGA CCTACAGAGA GGGCTCTTTG GTTTGAGGAC CATGGCTTAC CTTTCCTGCC	2400
	TTTGACCCAT CACACCCCAT TTCTCCTCT TCCCTCTCC CCGCTGCCAA TTCCTGCAGC	2460
20	CCGGGGGAAC CACTAGTT	2478

25 (2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

35	TGGCCTTGC TTTGTGGYC TTCTCTGTG GCCAGAGCGT TTTCATCACC AAGCCTCCTG	60
	ATGGCAGTNC CTTACCGAT ATGTTCAAGA TACTGACGTA TTCTGCTGT TCCAGAAGC	120
	GAAGTGAGA GCGCCAGAGT AATGGTGAAG GCATTGGAGT NTTTCAGCAA TCTTCTAAAC	180
40	AAAGTCTGTT TGATTATGT AAGATGTCTC ATGGTGGGCC ATTTACAGAA GAGAAAGTG	240
	AAGATGTGAA AGCTCTGGTC AAGATGTGCC CTGTTTTCTT GGCTTTGATA CCTTACTGGA	300
45	CAGTGTATTT CCAAATGCAG ACAACATATG TTTTACAGAG TCTTCATTTG AGGATTCCAG	360
	AAATTTCAAA TATTACAACC ACTCCTCACA CGCTCCCTGC AGCCTGGCTG ACCATGTTTG	420
	ATGCTGTGCT CATCCTCCTG CTCATCCCTC TGAAGGACAA ACTGGTCGAT CCCATTTTGA	480
50	GAAGACATGG CCGCTCCCA TCCTCCCTGA AGAGGATCGC CGTGGGCATG TTCTTTGTCA	540
	TGTGCTCRGC CTTGCTGCA GGAATTTTGG AGAGTAAAG GCTGAACCTT GTTAAAGAGA	600
55	AAACCATTAA TCAGACCATC GGCAACGTCG TCTACCATGC TGCCGATCTG TCGCTGTGGT	660
	GGCAGGTGCC GCAGTACTTG CTGATTGGGA TCAGCGAGAT CTTTGCAAGT ATCGCAGGCC	720
	TGGAATTTGC ATACTCAGCT GCCCCAAGT CCATGCAGAG TGCCATAATG GGCTTGTICT	780
60	TTTTCTTCTC TGGCGTCGGG TCGTTCGTGG GTTCTGGACT GCTGGCACTG GTGTCTATCA	840

AAGCCATCGG ATGGATGAGC AGTCACACAG ACTTTGGTAA TATTAACGGC TGCTATTTGA 900
 ACTATTACTT TTTCTTCTG GCTGCTATTC AAGGAGCTAC CCTCCTGCTT TTCCTCATTA 960
 5 TTTCTGTGAA ATATGACCAT CATCGAGACC ATCAGCGATC AAGAGCCAAT GCGGTGCCCA 1020
 CCAGCAGGAG GGCCTGACCT TCCTGAGGCC ATGTGCGGTT TCTGAGGCTG ACATGTCAGT 1080
 10 AACTGACTGG GGTGCACTGA GAACAGGCAA GACTTTAAAT TCCCATAAAA TGTCTGACTT 1140
 CACTGAAACT TGCATGTTGC CTGGATTGAT TTCTTCTTTC CCTCTATCCA AAGGAGCTTG 1200
 GTAAGTGCCT TACTGCAGCG TGTCTCCTGG CACGCTGGGC CCTCCGGGAG GAGAGCTGCA 1260
 15 GATTTCGAGT ATGTGCGTTG TCATTCAAGG TCTCTGTGAA TCCTCTAGCT GGGTTCCTTT 1320
 TTTTACAGAA ACTCACAAAT GGAGATTGCA AAGTCTTGGG GAACTCCACG TGTTAGTTGG 1380
 20 CATCCAGTT TCTTAAACAA ATAGTATCAC CTGCTTCCCA TAGCCATATC TCACTGTAAA 1440
 AAAAAAATT AATAAACTGT TACTTATATT TAAGAAAGTG AGGATTTTTT TTTTTTAAAG 1500
 ATAAAAGCAT GGTGAGATGC TGCAAGGATT TTACATAAAT GCCATATTTA TGGTTTCCTT 1560
 25 CCTGAGAACA ATCTTGCTCT TGCCATGTTT TTTGATTTAG GCTGGTAGTA AACACATTTT 1620
 ATCTGCTGCT TCAAAAAGTA CTTACTTTTT AAACCATCAA CATTACTTTT CTTTCTTAAG 1680
 30 GCAAGGCATG CATAAGAGTC ATTTGAGACC ATGTGTCCCA TCTCAAGCCA CAGAGCAACT 1740
 CACGGGTAC TTCACACCTT ACCTAGTCAG AGTGCTTATA TATAGCTTTA TTTTGGTACG 1800
 ATTGAGACTA AAGACTGATC ATGGTTGTAT GTAAGGAAAA CATTCTTTTG AACAGAAATA 1860
 35 GTGTAATTAA AAATAATTGA AAGTGTTAAA TGTGAAGTTG AGCTGTTTGA CCAGTCACAT 1920
 TTTTGTATTG TTAAGTACG TGTATCTGGG GCTTCTCCGT TTGTTAATAC TTTTCTGTGA 1980
 40 TTTGTGCTG TATTTTGGC ATAAGTTTAT TATAAAAAGC ATCTCAAATG CGAAAWAAAA 2040
 AAAAAAAAAA AAAAAAAC 2058

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(2) INFORMATION FOR SEQ ID NO: 92:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

GGCACAGGAG CGACCCGGGA GAAGGAGGGC CAMGAKGCGG AAGCGGAGGA GTCTCCAGGA 60
 60 GACCCGGGGA CAGCATCGCC CAGGCCCTG TTTGCAGGCC TTTCAGATAT ATCCATCTCA 120

	CAAGACATCC CCGTAGAAGG AGAAATCACC ATTCCTATGA GATCTCGCAT CCGGGAGTTT	180
	GACAGCTCCA CATTAAATGA ATCTGTTTCG AATACCATCA TCGTGATCT AAAAGCTGTT	240
5	GGGAAAAAAT TCATGCATGT TTTGTACCCA AGGAAAAGTA ATACTCTTTT GAGAGATTGG	300
	GATTTGTGGG GCCCTTTGAT CCTTGTGTG ACACTCGCAT TAATGCTGCA AAGAGACTCT	360
10	GCAGATAGTG AAAAAGATGG AGGGCCCCAA TTTGCAGAGG TGTTTGTCAT TGTCTGGTTT	420
	GGTGCACTTA CCATCACCTT CAACTCAAAA CTCTTGGAG GGAACATATC TTTTTTTCAG	480
	AGCCTCTGTG TGCTGGGTTA CTGTATACTT CCCTTGACAG TAGCAATGCT GATTTGCCGG	540
15	CTGGTACTTT TGGCTGATCC AGGACCTGTA AACTTCATGG TTCGGCTTTT TGTGGTGATT	600
	GTGATGTTTG CCTGGTCTAT AGTTGCCTCC ACAGCTTTCC TTGCTGATAG CCAGCCTCCA	660
20	AACCGCAGAG CCTAGCTGT TTATCCTGTT TTCCTGTTTT ACTTTGTCAT CAGTTGGATG	720
	ATCTCACCTT TACTCCTCA GTAAATCAGG AATGGGAAAT TAAAAACCAG TGAATTGAAA	780
	GCACATCTGA AAGATGCAAT TCACCATGGA GCTTTGTCTC TGGCCCTTAT TTGTCTAATT	840
25	TTGGAGGTAT TTGATAACTG AGTAGGTGAG GAGATTAAAA GGGAGCCATA TAGCACTGTC	900
	ACCCCTTATT TGAGGAACTG ATGTTTGAAA GGCTGTTCTT TTCTCTCTTA ATGTCATTTT	960
30	TTTAAAAATA CATGTGCATA CTACACACAG TATATAATGC CTCCTTAAGG CATGATGGAG	1020
	TCACCGTGGT CCATTGCGGT GACAACCACT GACTTGGGAA GCACATAGAT ACATCTTACA	1080
	AGTTGAATAG AGTTGATAAC TATTTTCAGT TTTGAGAATA CCAGTTCAGG TGCAGCTCTT	1140
35	AAACACATTG CCTTATGACT ATTAGAATAT GCCTCTCTTT TCATAAATAA AAATACATCG	1200
	TCTATATCCA TTTTCTTTTA TTTCTCTCTC TTAAGCTTAA AAAGGCAATG AGAGAGGTTA	1260
40	GGAGTGGGTT CATAACCGGA GAATGAGAAA ACATGCATTA ACCAATATTC AGATTTTGAT	1320
	CAGGGGAAAT TCTAYACTTG TTGCAAAAAA AAAAAAAAAA AAACCTCGAGG GGGGCCCGGT	1380
	ACCCAATCGC NGTATATGAT CGNAAACAAT C	1411

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(2) INFORMATION FOR SEQ ID NO: 93:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2187 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

60

GCTTTGGCTT TTTTGGCGG ACTGGGGCGC OCTCCGAAG CGTTTCCAAC TTTCCAGAAG	60
TTTCTCGGA CGGCAGGAG GGGTGGGA CTGCCATATA TAGATCCCGG GAGCAGGGGA	120

	GCGGGCTAAG AGTAGAATCG TGTCGCGCTC GAGAGCGAGA GTCACGTCCC GCGCTAGCC	180
5	CAGCCCGACC CAGGCCCACC GTGGTGCACG CAAACCACTT CCTGGCCATG CGCTCCCTCC	240
	TGCTTCTCAG CGCCTTCTGC CTCCTGGAGG CGGCCCTGGC CGCCGAGGTG AAGAAACCTG	300
	CAGCCGACG AGCTCCTGGC ACTGCGGAGA AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG	360
10	AGCGCAGCCG GCCTGGCCTT CAGCTTGTAC CAGGCCATGG CCAAGGACCA GGCAGTGGAG	420
	AACATCCTGG TGTCACCCGT GGTGGTGGCC TCGTCGCTGG GGCTCGTGTC GCTGGGCGGC	480
15	AAGGCGACCA CGGCGTCGCA GGCCAAGGCA GTGCTGAGCG CCGAGCAGCT GCGCGACGAG	540
	GAGGTGCACG CCGGCCCTGGG CGAGCTGCTG CGCTCACTCA GCAACTCCAC GCGCGCAAC	600
	GTGACCTGGA AGCTGGGCAG CCGACTGTAC GGACCCAGCT CAGTGAGCTT CGCTGATGAC	660
20	TTCTGTGCGA GCAGCAAGCA GCACTACAAC TCGGAGCACT CCAAGATCAA CTTCGCGAC	720
	AAGCGCAGCG CGCTGCAGTC CATCAACGAG TGGGCCGCGC AGACCACCGA CGGCAAGCTG	780
25	CCCGAGGTCA CCAAGGACGT GGAGCGCAGG GACGGCGCCC TGTTAGTCAA CGCCATGTTT	840
	TTCAAGCCAC ACTGGGATGA GAAATTCCAC CACAAGATGG TGGACAACCG TGGCTTCATG	900
	GTGACTCGGT CCTATACCGT GGGTGTCTATG ATGATGCACC GGACAGGCCT CTACAACCTAC	960
30	TACGACGACG AGAAGGAAAA GCTGCAAATC GTGGAGATGC CCCTGGCCCA CAAGCTCTCC	1020
	AGCCTCATCA TCCTCATGCC CCATCAGTGG GAGCCTCTCG AGCGCCTTGA AAAGCTGCTA	1080
35	ACCAAAGAGC AGCTGAAGAT CTGGATGGGG AAGATGCAGA AGAAGGCTGT TGCCATCTCC	1140
	TTGCCCAAGG GTGTGGTGA GGTGACCCAT GACCTGCAGA AACACCTGGC TGGGCTGGGC	1200
	CTGACTGAGG CCATTGACAA GAACAAGGCC GACTTGTAC GCATGTCAGG CAAGAAGGAC	1260
40	CTGTACCTGG CCAGCGTGT CCACGCCACC GCCTTTGAGT TGGACACAGA TGGCAACCTT	1320
	TTGACCAGAA TTACGGGCGG AGGAGTGCGC ACCCAAGTGT TCTACGCCGA CCACCCCTTC	1380
45	ATTTCTTAGT GCGGGACACC CAAAGCGGTC CCTGCTATTTC ATTGGGCGCC TGGTCCGGCC	1440
	TAAGGGTGAC AAGATGCGAG ACGAGTTATA GGCCTCAGGG TGCACACAGG ATGGCAGGAG	1500
	GCATCCAAAG GCTCCTGAGA CACATGGGTG CTATTGGGGT TGGGGGGGAG GTGAGGTACC	1560
50	AGCCTTGAT ACTCCATGGG GTGGGGTGA AAAGCAGACC GGGGTTCCTG TGTGCCTGAG	1620
	CGGACTTCCC AGCTAGAATT CACTCCACTT GGACATGGGC CCCAGATACC ATGATGCTGA	1680
55	GCCCGGAAAC TCCACATCCT GTGGGACCTG GGCCATAGTC ATTCTGCCTG CCCTGAAAGT	1740
	CCCAGATCAA GCCTGCCTCA ATCAGTATTTC ATATTATATAG CCAGGTACCT TCTCACCTGT	1800
	GAGACCAAAT TGAGCTAGGG GGGTCAGCCA GCCCTCTTCT GACACTAAAA CACCTCAGCT	1860
60	GCCTCCCAG CTCTATCCCA ACCTCTCCCA ACTATAAAAC TAGGTGCTGC AGCCCTGGG	1920

ACCAGGCACC CCCAGAATGA CCTGGCCGCA GTGAGGCGGA TTGAGAAGGA GCTCCCAGGA 1980
GGGGCTTCTG GGCAGACTCT GGTCAAGAAG CATCGTGTCT GGCCTTGTGG GGATGAACTT 2040
5 TTTGTTTTGT TTCTTCCTTT TTTAGTCTTT CAAAGATAGG GAGGGAAGGG GGAACATGAG 2100
CCTTTGTTGC TATCAATCCA AGAACTTATT TGTACATTTT TTTTTCAT AAACCTTTTC 2160
10 CAATGACAAA AAAAAAAAAA AAAAAA 2187

15 (2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 757 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

25 GACAGTACGG TCGGATTCCC GGGTCGACCC ACGCGTCCGC GGACGGTGAA GAAGGTGAAG 60
ATGGCGGTGG CCAGGGCCCG GTCTTGGA GTCCAGTGGC TGCAAAGGC ATCCCGGAAC 120
GTGATGCCGC TGGGCGCAGC GACAGCCTCC CACATGACCA AGGACATGTT CCCGGGGCCC 180
30 TATCCTAGGA CCCCAGAAGA ACGGGCCGCC GCCGCCAAGA AGTATAATAT GCGTGTGGAA 240
GACTACGAAC CTTACCCGGA TGATGGCATG GGGTATGGCG ACTACCGAA GCTCCCTGAC 300
35 CGCTCACAGC ATGAGAGAGA TCCATGGTAT AGCTGGGACC AGCGGGCCT GAGGTTGAAC 360
TGGGGTGAAC CGATGCACTG GCACCTAGAC ATGTACAACA GGAACCGTGT GGATACATCC 420
CCCACACCTG TTTCTTGGA TGTCATGTGT ATGCAGCTCT TCGGTTTCCT GGCTTTCATG 480
40 ATATTCATGT GCTGGGTGGG GGACGTGTAC CCTGTCTACC AGCCTGTGGG ACCAAAGCAG 540
TATCCTTACA ATAATCTGTA CCTGGAACGA GCGGTGATC CCTCCAAAGA ACCAGAGCGG 600
45 GTGGTTCACT ATGAGATCTG AGGAGGCTTC GTGGGCTTTT GGGTCCTCTA ACTAGGACTC 660
CCTCATTCCT AGAAATTTAA CCTTAATGAA ATCCCTAATA AAACCTAGTG CTGTGTTAAA 720
AAAAAAAAA AAAAAAAAAA AAAAAGGGGG GCCCCNN 757
50

55 (2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 2394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

5	GGCACGAGCA CTCCTGCACT TCCCCACCCC CACGACCGAA CCTGGCTTCG CTAACGCCCT	60
	CCCAGCTCCC TCGGCCTGA CTTCGGTTT CCTCGCGGT CCCTGGCGCC GAGCCGCGGA	120
	CAGCAGCCCC TTTTCGGCT GAGAGCTCAT CCACACTTCC AATCACTTTC CGGAGTGCTT	180
10	CCCCTCCTC CGGCCGTGC TGGTCCCGAC GCGGGGCTG GGTCTCGCGC GCGTATTGCT	240
	GGGTAACGGG CCTTCTCYCG CGTCGGCCCG GCCCCCTCTG CCTCGGCTCG TCCCTCCTTC	300
15	CAGAACGTCC CGGGCTCCTG CCGAGTCAGA AGAAATGGGA CTCCCTCCGC GACGTGCCCG	360
	GAGCAGCTCC CTTCGCTGTG GAAGCGGCGG TGTCTCGAA GAAACCGGAA GCCCGTGGTG	420
	ACCCCTCGCG ACCCGGTTTG TTTTCGGTCC GTTTCCAAAC ACTAAGGAAT CGAAACTCGG	480
20	CGGCCTTGGG GCGGCCCTA CGTAGCCTGG CTCTGGTTG TCATGGATGC ACTGGTAGAA	540
	GATGATATCT GTATTCTGAA TCATGAAAAA GCCCATAAGA GAGATACAGT GACTCCAGTT	600
25	TCAATATATT CAGGAGATGA ATCTGTGCT TCCCAITTTG CTCTGTTCAC TGCATATGAA	660
	GACATCAAAA AACGACTTAA GGATTTCAGAG AAAGAGAACT CTTTGTAAA GAAGAGAATA	720
	AGATTTTGG AAGAAAAGCT AATAGCTCGA TTGAAGAAG AAACAAGTTC CGTGGGACGA	780
30	GAACAAGTAA ATAAGGCTA TCATGCATAT CGAGAGGTTT GCATTGATAG AGATAATTG	840
	AAGAGCAAAC TGGACAAAAT GAATAAGAC AACTCTGAAT CTTTGAAAGT ATTGAATGAG	900
35	CAGCTACAAT CTAAGAAGT AGAACTCCTC CAGCTGAGGA CAGAGGTGGA AACTCAGCAG	960
	GTGATGAGGA ATTTAAATCC ACCTTCATCA AACTGGGAGG TGGAAAAGTT GAGCTGTGAC	1020
	CTGAAGATCC ATGGTTTGA ACAAGAGCTG GAACTGATGA GGAAAGAATG TAGCGATCTC	1080
40	AAAATAGAAC TACAGAAAGC CAAACAAACG GATCCATATC AGGAAGACAA TCTGAAGAGC	1140
	AGAGATCTCC AAAAATAAG CATTTCAAGT GATAATATGC AGCATGCATA CTGGGAAC TG	1200
45	AAGAGAGAAA TGTCTAATTT ACATCTGGTG ACTCAAGTAC AAGCTGAACT ACTAAGAAAA	1260
	CTGAAAACCT CAACTGCAAT CAAGAAAGCC TGTGCCCTG TAGGATGCAG TGAAGACCTT	1320
	GGAAGAGACA GCACAAAAC GCACTTGATG AATTTTACTG CAACATACAC AAGACATCCC	1380
50	CCTCTCTTAC CAAATGGCAA AGCTCTTTGT CATACCACAT CTTCCTTTT ACCAGGAGAT	1440
	GTAAAGGTTT TATCAGAGAA AGCAATCCTC CAATCATGGA CAGACAATGA GAGATCCATT	1500
55	CCTAATGATG GTACATGCTT TCAGGAACAC AGTTCTTATG GCAGAAATTC TCTGGAAGAC	1560
	AATTCCTGGG TATTTCCAAG TCCTCCTAAA TCAAGTGAGA CAGCATTTGG GGAAACTAAA	1620
	ACTAAAACCT TGCCTTACC CAACCTTCCA CCACTGCATT ACTTGGATCA ACATAATCAG	1680
60	AACTGCCTTT ATAAGAATTA ATTTGGAAGA GATTCACGAT TTCACCATGA GGACACTTAT	1740

CTCTTTTCAGT GGTCTCTCCA AGAAATTATT TAACAACTG AANGGAGATT TTGATTAAAA 1800
 TTTTGCAGAG GTCTTCAGTA TCTATATTG AACACACTGT ACAATAGTAC AAAAACCAAC 1860
 5 ATAGTTGGTT TTCTAGTATG AAAGAGCACC CTCTAGCTCC ATATTCTAAG AATCTGAAAT 1920
 ATGCTACTAT ACTAATTAAT AAGTAACTT AAGGTGTTTA AAAAAGCTCTG CCTTCTATAT 1980
 10 TAATTGTAAA ATTTTGCCTC TCAGAAGAAT GGAATTGCAG ATTGTAGACG TGGTTTACAA 2040
 AAATGTGAAA TGTCTAAATA TCTGTTTATA AAAATAAAAG GAAAACATGT TTCTTCAAAT 2100
 TGCATAATGG AACAAATGGC AATGTGAGTA GGTACATTT CTGTTGTTAT AATGCGTAAA 2160
 15 GATATTGAAA ATATAATGAA ATAAAAGCAT CTTAGGTTAT ACCATCTTTA TATGCTATTG 2220
 CGTTTCAATA TTTAAGATTT AAAGTGATTT TTTGGTCACA GTGTTTGTGTT GATAAAATTT 2280
 20 TTTTAGAATT GAAGTTTGAA TTCTAAGACT TGAAACAACC TGATCACTGA AGCCAACTTT 2340
 GTCCAGCAC ATTCCTTAAG TCCTAATTGG GGAAAAAAA AAAAAAAAC TCGA 2394

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(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGTGCTCTGT TGCCAGGCT GGAGTGCCTT AGTGTAATGT CAGTCCACTG CAACCTCCAC 60
 CCCAGGTTT AAGCAATTCT CATGCCICAG CCTCCAAGT AGCTGAAAT ACTGGCATGC 120
 40 ACCACCACAC CCAGCTGATG TTTATTTATT TATTTATATA TTTATTTATT TTAGGTGTTT 180
 TTTTTTTTTT TTTTGAGAC GGAGTCTGTC TCTGTTGCCC TGGGTGTGGT TACGTGGRAT 240
 45 TACCATYCTG GGTGACTCAC TGAAATGTAC TCMCAGTGAG TCATGCCTTC MAATGACATC 300
 TCAAGTCTG CCTGCTTGA GATACATCTG GGGATCTTAA GGGGTGAGG ACTACTCAAC 360
 AAGAAGGAAT TTAGCCTGTC TTTTAAATA AACGGCATT CTTTTCCTA KAAAAATGGG 420
 50 AAATCTTCA ATTCTCTAAT ACAGGGACAC TGAGATAACA AAGAGGAAAG TGTCTGGTTG 480
 GAGGTTGGGA RGCCACCCTG GGGTCTCTCC TACAAAAATG GAAAAGAAAA GAACGGTGAR 540
 55 AAATCMAGCA AAGCACAARA AAKTTTCCCT TTGCTAAAAG GGAAAAGATG CCCCMAATG 600
 CCCATAAACA TGAAGTGGG ATAAGGAGGA RAATGTCTCT YCTTGGCACC CCCAAACAAA 660
 CGTTAATTAC CC 672
 60

(2) INFORMATION FOR SEQ ID NO: 97:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1419 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

15	TAAGAACAGA ACAGCAAGTA TGAACCACAT GGAACCTAAA ACATATGGGT GTGAAGTCCA	60
	CTTATGTAGA CAAAACCTAT AATTTCCTAA CTGTTGTCTA GTATACAGTG ATCAGTTGCT	120
	CTCTGTTCAA GTCATTCCAC ACATTTCCCT ATTTTAGGCT ATTATAATAT AGAAAGAAAA	180
20	TGGGAAGCAT TAGTTGGAGC TAGAAAATGA ACTGTATATT ATTGCTATAT TTGCTAATAC	240
	CAACTATTTC AATAAGTGTT GTACCATATG TAGCATTAAA TATAAAATAC ATAAAAGAAT	300
	GTACAGAAAA TAGCTTTTAT TGAGTAATAT TACATTTTCAT TTATACTGTA GCAATATATT	360
25	TGTAGGTATA CTCTGTAAGG GCTTTAAATA AAAGAGGTCC ATTAATACTT CCTTATAAAA	420
	ATTCTAGTCT GTTTCATTAC TGCCCAGATG TTTTAGAGAT AAATATTTAT GCAGAAGGTA	480
30	TTTTCGAAAG TCYCCYTTTG TCTGATAGAG TTTAACNAGA TATTTAAATT TAGTGCYCNA	540
	GAAATCCAC AAGTCACGGT CTAACACAC TTAGAATACT ACAGCATAAA TCTGTTAGCA	600
	TTANITGCCA AATAAGACAG TTGGGATCCC AAACCCCAAG TCCTTGAGCA ATGTTTTTCC	660
35	TCAAAAAGCT GCTATNCCAA TGATATAGGA AAAWACATG TGTTCCTTA AACACACTTT	720
	TCTTTTTAAA TGTGCTTCAT TGTTCGATTT GGTCTGCCT AAATTCACA AGCTAGGCCA	780
40	ATGAAGGCTG AATCAAAGAC ATTTTCATCCA CCAATATCAT GTGTAGATAT TATGTATAGA	840
	AAATAAAATA AATTATGGCT CTAACCTCTG TGTTGCTGTT TATCTTGTTA TTTTCGGCG	900
	TTATACTAAT GNGTTTATTG AGAGCATTTT ACCTTCAGA CTTCTCATGG CTAACTTTTG	960
45	GTCTGWATTT TGSTCCTTAG ATGKGAATAT TTCTTATTAG TYTGCTYCCT GCWACGCAAT	1020
	GACTGCATTT CTATCATTTT TCAGTTTGTT AGWATATGTG GATAGTATTC TACTGTATAA	1080
50	ATGATTGCAA AGTTTATCAA AAACAAATTA TTATATGTAG CTTTTCTACA GTGCTTTGCT	1140
	AAACCATGTA GTACTAGTTA AGTSTTCCTT GAAAATAAAG ATACACTCTT ATAGGGGACA	1200
	GTTCTCTGTT ACTCCCAGGA AACTTTTTTA AAAGATGACA CTGAATGTTT ATTGCACTTT	1260
55	AGTGCACTGA AGTGGCAATA AAACCTAACA TGAATCAAGG TTGTTTATGG CAGATGCATG	1320
	TGTTGCTTTA CAGAGTTTAG CAAAAGCTCT TAATTTTATG TCATACTGTA TTCTACTGAA	1380
60	TAATAAAGCT AACATTATTC AATAATAAAA TGGAAAAA	1419

5 (2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

15 GCGACCGCGC CCCTTTCAGC TAGCTCGCTC GCTCGCTCTG CTTCCCTGCT GCCGGCTGCG 60
CATGGCKWTG GCGTTGGCGG CGCTGGCGGC GGTGAGCCG GCCTGCGCAG CCGGTACCAG 120
CAGTTGCAGA ATGAAGAAGA GTCTGGAGAA CCTGAACAGG CTGCAGGTGA TGCTCCTCCA 180
20 CCTTACAGCA GCATTCTCTC AGAGAGCGCA GTTTTCCACC TATTTCCCTG GATATTTTGA 240
TGGTCAGTAC TGGCTCTGGT GGGTGTTCCT TGTMTTAGGC TTTCTCCTGT TTCTCAGAGG 300
25 ATTTATCAAT TATGCAAAG TTCGGAAGAT GCCAGAACT TTCTCAAATC TCCCCAGGAC 360
CAGAGTCTC TTTATTTATT AAAGATGTTT TCTGGCAAAG GCCTTCCTGC ATTTATGAAT 420
TCTCTCTCAA GAAGCAAGAG AACACCTGCA GGAAGTGAAT CAAGATGCAG AACACAGAGG 480
30 AATAATCACC TGCTTTAAAA AAATAAAGTA CTGTTGAAAA GATCATTTCT CTCTATTTGT 540
TCCTAGGTGT AAAATTTTAA TAGTTAATGC AGAATCTGT AATCATTGAA TCATTAGTGG 600
35 TTAATGTTTG AAAAAGCTCT TGCAATCAAG TCTGTGATGT ATTAATAATG CCTTATATAT 660
TGTTTGTAGT CATTTTAAGT AGCATGAGCC ATGTCCCTGT AGTCGGTAGG GGGCAGTCTT 720
GCTTTATICA TCCTCCATCT CAAAATGAAC TTGGAATTAA ATATTGTAAG ATATGTATAA 780
40 TGCTGGCCAT TTTAAAGGGG TTTCTCAAA AGTTAACTT TTGTTATGAC TGTGTTTTTG 840
CACATAATCC ATATTGCTG TTCAAGTTAA TCTAGAAATT TATTCAATTC TGTATGAACA 900
45 CCTGGAAGCA AAATCATAGT GCAAAAATAC ATTTAAGGTG TGGTCAAAAA TAAGTCTTTA 960
ATTGGTAAAT AATAAGCATT AATTTTTTAT AGCCTGTATT CACAATCTG CGGTACCTTA 1020
TTGTACCTAA GGGATTCTAA AGGTGTTGTC ACTGTATAAA ACAGAAAGCA CTAGGATACA 1080
50 AATGAAGCTT AATTACTAAA ATGTAATTCT TGACACTCTT TCTATAATTA GCGTCTTCA 1140
CCCCACCCC CACCCCACC CCCCTATTT TCCTTTTGTG TCCTGGTGAT TAGGCCAAAG 1200
55 TCTGGGAGTA AGGAGAGGAT TAGGTACTTA GGAGCAAAGA AAGAAGTAGC TTGGAACTTT 1260
TGAGATGATC CCTAACATAC TGTACTACTT GCTTTTACAA TGTGTTAGCA GAAACCAGTG 1320
GGTTATAATG TAGAATGATG TGCTTCTGTC CCAAGTGGTA ATTCATCTTG GTTTGCTATG 1380
60

TTAAACTGT AAATACAACA GAACATTAAT AAATATCTCT TGTGTAGCAC CTTTAAAAAA 1440
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAN CCCGGGGGGG GGCCCN 1487

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(2) INFORMATION FOR SEQ ID NO: 99:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1653 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GCGACCGCGC CCTTCAGCTA GCTCGCTCGC TCGCTCTGCT TCCCTGCTGC CGGCTGCGCA 60
 20 TGGCTTNGGC GTTGGCGGCG CTGGCGGCGG CTCGAGCCGC CTGCGSAGCC GGTACCAGCA 120
 GTTGCAGAAT GAAGAAGAGT CTGGAGAACC TGAACAGGCT GCAGGTGATG CTCCTCCACC 180
 25 TTACAGCAGC ATTCTGCAG AGAGCGCACA TNATTTTGAC TACAAGGATG AGTCTGGGTT 240
 TCCAAAGCCC CCATCTTACA ATGTAGCTAC AACACTGCCC AGTTATGATG AAGCGGAGAG 300
 GACCAAGGCT GAAGCTACTA TCCCTTTGGT TCCTGGGAGA GATGAGGATT TTGTGGGTCG 360
 30 GGATGATTTT GATGATGCTG ACCAGCTGAG GATAGGAAAT GATGGGATTT TCATGTTAAC 420
 TTTTTCATG GCATTCCTCT TTAACGGAT TGGGTTTTTC CTGTCTTTTT GCCTGACCAC 480
 TTCAGCTGCA GGAAGGTATG GGGCCATTTT AGGATTTGGT CTCTCTCTAA TTAAATGGAT 540
 35 CCTGATTGTC AGGTTTTCCA CCTATTTCCC TGCATTTATG AATCTCTCTT CAAGAAGCAA 600
 GAGAACACCT GCAGGAAGTG AATCAAGATG CAGAACACAG AGGAATAATC ACCTGCTTTA 660
 40 AAAAAATAAA GTACTGTTGA AAAGATCATT TCTCTCTATT TGTTCCTAGG TGTAAATTT 720
 TAATAGTTAA TGCAGAATTC TGTAAATCATT GAATCATTAG TGGTTAATGT TTGAAAAGC 780
 TCTTGCAATC AAGTCTGTGA TGTATTAATA ATGCCTTATA TATTGTTTGT AGTCATTTTA 840
 45 AGTAGCATGA GCCATGTCCC TGTAGTCGGT AGGGGGCAGT CTTGCTTTAT TCATCCTCCA 900
 TCTCAAAATG AACTTGAAT TAAATATTGT AAGATATGTA TAATGCTGGC CATTTTAAAG 960
 50 GGGTTTCTC AAAAGTTAAA CTTTGTGTTT GACTGTGTTT TTGCACATAA TCCATATTTG 1020
 CTGTTCAGT TAATCTAGAA ATTTATTCAA TTCTGTATGA ACACCTGGA GCAAATCAT 1080
 AGTGCAAAAA TACATTTAAG GTGTGGTCAA AAATAAGTCT TTAATTGGTA AATAATAAGC 1140
 55 ATTAATTTTT TATAGCCTGT ATTCACAATT CTGCGGTACC TTATTGTACC TAAGGGATTC 1200
 TAAAGGTGTT GTCACGTAT AAAACAGAAA GCACTAGGAT ACAAATGAAG CTTAATTACT 1260
 60 AAAATGTAAT TCTTGACACT CTTTCTATAA TTAGCGTTCT TCACCCCCAC CCCCACCCC 1320

ACCCCCTTA TTTTCCTTTT GTCTCCTGGT GATTAGGCCA AAGTCTGGGA GTAAGGAGAG 1380
 GATTAGGTAC TTAGGAGCAA AGAAAGAAGT AGCTTGAAC TTTTGAGATG ATCCCTAACA 1440
 5 TACTGTACTA CTTGCTTTTA CAATGTGTTA GCAGAAACCA GTGGGTTATA ATGTAGAATG 1500
 ATGTGCTTTC TGCCCAAGTG GTAATTCATC TTGGTTTGCT ATGTTAAAAC TGTAATACA 1560
 10 ACAGAACATT AATAAATATC TCTGTGTAG CACCTTTTAW AAAAAAAAAA AAAAAAAAAA 1620
 AAAAAAAAAA AAAANCCCG GGGGGGGGCC CCN 1653

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(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 1145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TTTTTTTTTT TTTTTTTTTT TTGACTGAAC TAAGTGGCTT TTTTATTAGA GAAAGCCAGA 60
 ATTACAAAG ACTTCCCTTT TCTTGGGGTA TGGCTGTCTC AGCACAATAC TCAACATAAC 120
 30 TGCAGAACTG ATGTGGCTCA GGCACCCTGG TTTTAATTCC TTGAGGATCT GGCAATGGC 180
 TTACGCAAAA GGTCAACATT TGAGGTCCTG CCTTACTAAT TATGTGCTGC CCAACAATA 240
 35 AATTGTAAAT TTGTTTTTCT CTAGTTTGAG CAGGGTCTGA ATTTTTTCAT TTATTTCTTT 300
 TTTTGCCAGC AGACAGACTT GAGTCTGTAA AGACAAGCAA ATACACTGAC AGAAGTTTAC 360
 CATAGTTTCT AAAATGTAAA AAAGAAAACC CCCAAAAGAC TCAAGAAAAT TAGACCACAA 420
 40 ATTTTGCATT GTTCATTGTA GCACTATTGG TAATAAAATA ACAAATGTTT GTGCATTTTT 480
 ATGTGAAGAT CCTTCTCGTA TTTCAATTGG AAAGATGAGC AAGAGGTCTG CTTCCTTCAT 540
 45 TTTACTTCCC CTTCTGTTTT TGAAAGGCAG TTTCGCCAAG CTTAATGCAA GAATATCTGA 600
 CTGTTTAGAA GAAAGATATT GCCACAATCT CTGGATGGTT TTCCAGGGTT GTGTTATTAC 660
 TGAGCTTCAT CTTTCCAGAA TGAGCAAAAC ACTGTCCAGT CTTTGTACG ATTTGTAAAT 720
 50 AAATGTGTAC ATTTTTTTTA AATTTTTGGA CATCACATGA ATAAAGGTAT GTATGTACGA 780
 ATGTGTATAT ATTATATATA TGACATCTAT TTGGAAAAT GTTTGCCCTG CTGTACCTCA 840
 55 TTTTATAGGAG GTGTGCATGG ATGCAATATA TGAAATGGG ACATTCTGGA ACTGCTGGTC 900
 AGGGGACTTT GTCGCCCTGT GCACTAAAAG GGCCAGATTT TCAGCAGCCA AGGACATCCA 960
 TACCCAAGTG AATGTGATGG GACTTAAAAG AAGTGAAGTG AGACAATTCA CTCTGGCTGT 1020
 60

TTGAACAGCA GCGTTTCATA GGAAGAGAAA AAAAGATCAA TCTTGTATTT TCTGACCACA 1080
TAAAGGCTTC TTCTCTTTGT AATAAAGTAG AAAAGCTCTC CTCAAAAAAA AAAAAAAAAA 1140
5 AAAAA 1145

10 (2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 734 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

20 TACCCGGCGG ATTCCAGGAA GGTAAATTTA GTCCTATAAT TTTCAGCTTA ATTATAAACA 60
AAGGAACAAA TAAGTGAAG GGCAGCTATT ACCATTGCT TAGTCAAAAC ATTCCGGTTAC 120
TGCCCTTTAA TACACTCCTA TCATCAGCAC TTCCACCATG TATTACAAGT CTGACCCAT 180
25 CCCTGTCGTA ACTCCAGTAA AAGTTACTGT TACTAGAAAA TTTTATCAA TTAAGTGACA 240
AATAGTTTCT TTTTAAAGTA GTTCTTCCA TCTTTATTCT GACTAGCTTC CAAAATGTGT 300
30 TCCCTTTTGT AATCGAGGTT TTTTGTGTTT GTTTGTGTTT CTGAAAAAT CATACAACTT 360
TGTCCTTCTA TTGCTTTTGT GTGTTTGTGTT AAGCATGTCC CTGCGCCCA ATGGAAGAGG 420
AAATGTTTAA TTAATGCTTT TTAGTTTAAA TAAATTGAAT CATTTATAAT AATCAGTGTT 480
35 AACAAATTTAG TGACCCTTGG TAGGTTAAAG GTTGCATTAT TTATACTTGA GATTTTTC 540
CCCTAACTAT TCTGTTTGT GTACTTTAAA ACTATGGGG AAATATCACT GGTCTGTCAA 600
40 GAAACAGCAG TAATTATTAC TGAGTTAAAT TGAAAAGTCC AGTGACCAG GCATTTCTTA 660
TATAAATAAA ATTGGTGGTA CTAATGTGAA AAAAAAAAAA AAAAAAACT CGAGGGGGGC 720
45 CCGGTACCCT ATTA 734

50 (2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

60 CCGCGGAAC GCTGTCCTGG CTGCCGNCAC CCGAACAGCC TGTCTGCTG CCCC GGCTCC 60

CTGCCCCGCG CCCAGTCATG ACCCTGCGCC CCTCACTCCT CCCGCTCCAT CTGCTGCTGC 120
 TGCTGCTGCT CAGTGC GCGG GTGTGCCGGG CTGAGGCTGG GCTCGAAACC GAAAGTCCCG 180
 5 TCCGGACCCT CCAAGTGGAG ACCCTGGTGG AGCCCCCAGA ACCATGTGCC GAGCCCGCTG 240
 CTTTGGGAGA CACGCTTCAC ATACACTACA CGGGAAGCTT GGTAGATGGA CGTATTATTG 300
 ACACCTCCCT GACCAGAGAC CCTCTGGTTA TAGAACTTGG CCAAAGCAG GTGATTCCAG 360
 10 GTCTGGAGCA GAGTCTTCTC GACATGTGTG TGGGAGAGAA GCGAAGGGCA ATCATTCCTT 420
 CTCACTTGGC CTATGGAAAA CGGGATTTC CACCATCTGT CCCAGCGGAT GCAGTGGTGC 480
 15 AGTATGACGT GGAGCTGATT GCACTAATCC GAGCCAACTA CTGGCTAAAG CTGGTGAAGG 540
 GCATTTTGCC TCTGGTAGGG ATGGCCATGG TGCCACCCTC CTGGGCCTCA TTGGGTATCA 600
 CCTATACAGA AAGGCCAATA GACCCAAAGT CTCCAAAAG AAGCTCAAGG AAGAGAAACG 660
 20 AAACAAGAGC AAAAAGAAAT AATAAATAAT AAATTTTAAA AAACITAAAA AAA 713

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(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

35

CCGATGTGGA CATCATCTG TCTATCCCA TGTTCCTGCG CCTGTACCTG ATCGCCCGAG 60
 TCATGCTGCT GCACAGAAGC TCTTCACCGA TGCTCTGCTC CGCAGCATCG GGGCCCTCAA 120
 40 CAAGATCAAC TTCAACCCC GCTTTGTCAT GAAGACGCTC ATGACCATCT GCCCTGGCAC 180
 TGTGCTGCTC GTGTTACGCA TCTCTCTGTG GATCATTGCT GCCTGGACCG TCCGTGTCTG 240
 TGAAAGTCCT GAATCACCAG CCCAGCCTTC TGGCTCATCA CTTCCTGCTT GGTACCATGA 300
 45 CCAGCAGGAC GTAAGTAGTA ACTTTCTGGG TGCCATGTGG CTCATCTCCA TCACATTCTT 360
 TTCCATTGGT TATGGGGACA TGGTGCCCA CACATACTGT GGGAAAGGTG TCTGTCTCCT 420
 50 CACTGGCATC ATGGGTGCAG GCTGCACTGC CCTTGTGGTG GCCGTGGTGG CCCGAAAGCT 480
 GGAATCACC AAAGCGGAGA AGCACGTTCA TAANITCATG ATGGACACTC AGCTCACCAA 540
 GCGGATCAAG AATGYTGAG CCAATGTCCT TSGGGAAACA TGGTTAATCT ATAAACACAC 600
 55 AAAGYGYTA AAGAAGATTG ACCATGCCAA AGTGAGGAAC ACCAGAGGAA GTTCYTCCAA 660
 GTATCCACCA GTTGAGGAGC GTCAAGATGG AACAGAGGAA GCTGAGTGAC CAAGCCAACA 720
 60 NICTGGTGGA CCTTTCCAAG ATGCAGAATG TCMGTATGA CTTAATCACA GAACTCAATG 780

ACCGGAGCGA AGACCTGGAG AAGCAGATTG GCAGCCTGGA GTCGAAGCTG GAGCATCTCA 840
 5 CCGCCAGCTT CAACTCCCTG CCGCTGCTCA TCGCCGACAC CCTGCGCCAG CAGCAGCAGC 900
 AGTCCTGTG TGCCATCATC GAGGCCCGGG GTGTCAGCGT GGCAGTGGG ACCACCCACA 960
 CCCCAATCTC CGATAGCCCC ATTGGGGTCA GCTCCACCTC CTTCCCGACC CCGTACACAA 1020
 10 GTTCAAGCAG TTGCTAAATA AATCTCCCCA CTCCAGAAGC ATTAAAAAA AAAAAAAAAA 1080

15 (2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 489 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

25 GGCACGAGAG GCTTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT CACCACCATG 60
 AAGTCTTAG CAGTCCTGGT ACTCTGGGA GTTCCATCT TTCTGGTCTC TGCCCAGAAT 120
 30 CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGCTGA TGATGAAGCC 180
 CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC TACCACTGCA 240
 ACCACCGCTG CTTCTACCAC TGCTCGTAAA GACATTCCAG TTTTACCCAA ATGGGTMTGG 300
 35 GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT TCTGCAATTG 360
 GTCACAAC TAATGCTTC CTGTGATTTC ATCCAAC TACCTTGCC TACGATATCC 420
 40 CCTTATCTC TAATCAGTTT ATTTCTTTC AAATAAAAAA TAACTATGAG CAACAAAAA 480
 AAAAAAAA 489

45

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 640 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

55 GCGGTCGCGC CTGTTGTTGT GGTCCCCATG GAGCTGCCGT AGCGGACCCA GCACAGCCAG 60
 GAGCGTCCGG GATGAGCTCA GCGCGGCCG ACCACTGGGC GTGGTTGCTG GTGCTCAGCT 120
 60 TCGTGTGTTG ATGCAATGTT CTTAGGATCC TCCTCCCGTC CTTCTCATCC TTCATGTCCA 180

GGGTGCTGCA GAAGGACGCG GAGCAGGAGT CACAGATGAG AGCGGAGATC CAGGACATGA 240
 AGCAGGAGCT CTCCACAGTC AACATGATGG ACGAGTTTGC CAGATATGCC AGGCTGGAAA 300
 5 GAAAGATCAA CAAGATGACG GATAAGCTCA AAACCCATGT GAAAGCTCGG ACAGCTCAAT 360
 TAGCCAAGAT AAAATGGGTG ATAAGTGTCT CTTTCTACGT ATTGCAGGCT GCCCTGATGA 420
 10 TCTCACTCAT TTGGAAGTAT TATTCTGTCC CTGTGGCTGT CGTGCCGAGT AAATGGATAA 480
 CCCTYTAGAC CGCTGGTAG CCTTTCCYAY TAGAGTAGCA GGTGGTGTGT GAATTACTGT 540
 TGGATTTART CTGTACAAAT TGTCCTATTG TGCTTCACCG TYCASTGAAC AGGAGGTGGT 600
 15 ACAGCCGGAG TTA AAAACGG TTCCNTTCC AGTTTAAAT 640

20

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 1529 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

30

GGGCACNAGA TGGAGCTGCC GTAGCGGACC CAGCACAGCC AGGAGCGTCC GGGATGAGCT 60

CAGCCGCGGC CGACCACTGG GCGTGGTTGC TGGTGCTCAG CTTCTGTGTT GGATGCAATG 120

35

TTCTTAGGAT CCTCCTCCCG TCCTTCTCAT CCTTCATGTC CAGGGTGCTG CAGAAGGACG 180

CGGACAGGAG TCACAGATGA GAGCGGAGAT CCAGGACATG AAGCAGGAGC TCTCCACAGT 240

40

CAACATGATG GACGAGTTTG CCAGATATGC CAGGCTGGAA AGAAAGATCA ACAAGATGAC 300

GGATAAGCTC AAAACCCATG TGAAAGCTCG GACAGCTCAA TTAGCCAAGA TAAATGGGT 360

GATAAGTGTC GCTTCTACG TATGTCAGGC TGCCCTGATG ATCTCACTCA TTTGGAAGTA 420

45

TTATTCTGTC CCTGTGGCTG TCGTGCCGAG TAAATGGATA ACCCTCTAG ACCGCCGGT 480

AGCCTTTCCT ACTAGAGTAG CAGGTGGTGT TGGAATTACC TGTGGATTT TAGTCTGTAA 540

50

CAAAGTTGTC GCTATTGTGC TTCATCCGTT CAGCTGAACA GGAGGATGGA TACAGCCGCG 600

AGTAAAAAA CGGATTTCTT CTTCTAGCT TAAATCTGA TTTACACTGT TTTGTTTTTT 660

AAGAAACAAA AGTGCATAGT TTAGATTTTT TTTTGTGTA ATATGTTTGT TCTTGGACTT 720

55

TATGAGATAG TCTTATAAGA ATCAGATTT TCTACACCTG TCATTGAGCC AAGAAAGTCC 780

AGTTTATGAC ACGTATGTAC TAGTGAACAC CGTCCTCGAT CTGTACGAAA TGTGAAATGT 840

60

TTAGGGACAT CTCCATGCTG TCACTTGIGA TTTGCCCTCT TATGTATTTT GGTCAATATTG 900

	CCAAGTGGAA AGTCAAAATT TTCTAACAAC TTTAAGTAAG TTCTTTGAAG ACTTAGTGCT	960
	GTTTITAATC CAGTTTAGAA AGTAACITAA TTTTAATACC RCTACTAAAA ATTGAAAAAT	1020
5	TTCTTCTTTA ATCACATTCA ATATGGTTAA AAGAACAACA CTAATTGACA TTGCGTGGGC	1080
	TTTTTCTCCC TTTGTTTAAA ATGTCATTTG TTGAGCAAGA GTTGTATAGT ATTATCTACT	1140
10	TACTTGAGGC TGTTAATTTT TCATTACAGT GTTTTGTAAG TGTATCCACG AGACCATGAT	1200
	GCATTGTTTT GTGCTCAACT TGTGTTTGT ATTTAAAGCA TTTTGAATGA AGTGTATTTT	1260
	ATAAGCATTT AATATTTATG CTCCTTAGAA TGGAACACAG AAAACAAACC TTATAAGTCC	1320
15	TGATTAATCT GAACCAATAA CCTGTGTGGC CTACAAAGTA TAATTCATTT AAATGTTTCT	1380
	TAAACACATT TTTTCTAATT AAAATCTTTG CAAATGCTTG TGTAACTTCC TGCCTTACAG	1440
20	CTACTTGTTT GCTGTGAGCC ACCCGCAACT GACAAGTGGC TGTTAACTGA GTCACCATAT	1500
	CCCAGTAAAG CTGAATTTTC TCACTAAAA	1529

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(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

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	ATGAAGGGTC GTTGGTGGGA AAGATGGCGG CGACTCTGGG ACCCCTTGGT CGTGGCAGCA	60
	GTGGCGRCGA TGTTGTTCGG CTCGGGATGG GTCCAGGATG TTAATCCTTC TTCTTTTGT	120
40	GGGCTCTGGG CAGGGGCCAC AGCAAGTCGG GCGGGTCAA ACGTTCGAGT ACTTGAAACG	180
	GGAGCACTCG CTGTGGAAGC CCTACCAGGG TGTGGGCACA GGCAGTTCCT CACTGTGGAA	240
45	TCTGATGGGC AATGCCATGG TGATGACCCA GTATATCCGC CTTACCCAG ATATGCAAAG	300
	TAAACAGGGT GCCTTGTGGA ACCGGGTGCC ATGTTTCTTG AGAGACTGGG AGTTGCAGGT	360
	GCACTTCAAA ATCCATGGAC AAGGAAAGAA GAATCTGCAT GGGGATGGCT TGGCAATCTG	420
50	GTACACAAAG GRWTCGGATG CAGCCAGGGC CTGTNTTTGG GAAACATGGA CAAATTTGTG	480
	GGGCTGGGAG TATTTGTAGA CACCTACCCC AATGAGGAGA AGCAGCAAGA GCGGGTATTC	540
55	CCCTRCMTCT CAGCCATGGT GAACAACGGC TCCCTCAGCT ATGATCATGA GCGGGATGGG	600
	CGGCCTACAG AGCTGGGAGG CTGCASAGCC ATGTTCGCA ATCTTCATTA CGACACCTTC	660
	CTGGTGATTC GCTACGTCAA GAGGCATTTR ACGATAATGA TGGATATTGA TGGCAAGCAT	720
60	GAGTGGAGGG ACTGCATTGA AGTGCCCGGA GTCCGCCTGC CCCGCGGCTA CTACTTCGGC	780

	ACCTCCTCCA TCACTGGGGA TCTCTCAGAT AATCATGATG TCATTTCTCTT GAAGTGTGTTT	840
5	GAAGTACAG TGGAGAGAAC CCCAGAAGAG GAAAAGCTCC ATCGAGATGT GTTCTTGCCC	900
	TCAGTGGACA ATATGAAGCT GCCTGAGATG ACAGCTCCAC TGCCGCCCCCT GAGTGGCCTG	960
	GCCCTCTTCC TCATCGTCTT TTTCTCCCTG GGTGTTTTCT GTATTTGCCA TAGTCATTGG	1020
10	TATCATACTC TACAACAAAT GGCAGGAACA GAGCCGAAAG CGCTTCTACT GAGCCCTCCT	1080
	GCTGCCACCA CTTTGTGTAC GTGCACCCAT GAGGTATGGA AGGAGCAGGC ACTGGCCTGA	1140
15	GCATGCAGCC TGGAGAGTGT TCTGTCTCTT AGCAGCTGGT TGGGGACTAT ATTCTGTAC	1200
	TGGAGTTTGT AATGCAGGGA CCCCAGATTC CCATGGTTGT GCATGGGGAC ATCTAACTCT	1260
	GGTCTGGGAA GCCACCCACC CCAGGGCAAT GCTGCTGTGA TGTGCCCTTC CCTGCAGTCC	1320
20	TTCCATGTGG GAGCAGAGGT GTGAAGAGAA TTTACGTGGT TGTGATGCCA AAATCACAGA	1380
	ACAGAATTTC ATAGCCCAGG CTGCCGTGTT GTTTGACTCA GAAGGCCCTT CTACTTCAGT	1440
25	TTTGAATCCA CAAAGAATTA AAACTGGTA ACACCACAGG CTTTCTGACC ATCCATTCTG	1500
	TGGGTTTTCG ATTTGACCCA ACCCTCTGCC TACCTGAGGA GCTTTCTTTG GAAACCAGGA	1560
	TGGAAACTTC TTCCCTGCCT TACCTTCCTT TCACTCCATT CATTGTCTCT TCTGTGTGCA	1620
30	ACCTGAGCTG GGAAAGGCAT TTGGATGCCT CTCTGTGGG GCCTGGGGCT GCAGAACACA	1680
	CCTGCGTTTC ACTGGCCTTC ATTAGGTGGC CCTAGGGAGA TGGCTTCTG CTTTGGATCA	1740
35	CTGTTCCTTA GCATGGGTCT TGGGTCTATT GGCATGTCCA TGGCCTTCCC AATCAAGTCT	1800
	CTTCAGGCCC TCAGTGAAGT TTGGCTAAAG GTTGGTGTAA AAATCAAGAG AAGCCTGGAA	1860
	GACATCATGG ATGCCATGGA TTAGCTGTGC AACTGACCAG CTCCAGTTT GATCAAACCA	1920
40	AAAGCAACAT TTGTCATGTG GTCTGACCAT GTGGAGATGT TTCTGGACTT GCTAGAGCCT	1980
	GCTTAGCTGC ATGTTTTGTA GTTACGATTT TTGGAATCCC ACTTTGAGTG CTGAAAGTGT	2040
45	AAGGAAGCTT TCTTCTTACA CCTTGGGCTT GGATATTGCC CAGAGAAGAA ATTTGGCTTT	2100
	TTTTTTNCTT AATGGACAAG AGACAGTTGC TGTCTCATG TTCCAAGTCT GAGAGCAACA	2160
	GACCCTCATC ATCTGTGCCT GGAAGAGTTC ACTGTCTATG AGCAGCACAG CCTGAGTGCT	2220
50	GGCCTCTGTC AACCTTATT CCACTGCCTT ATTTGACAAG GGGTTACATG CTGCTCACCT	2280
	TACTGCCCTG GGATTAAATC AGTTACAGGC CAGAGTCTCC TTGGAGGGCC TGGAACCTCTG	2340
55	AGTCCTCCTA TGAACCTCTG TAGCCTAAAT GAAATTCTTA AAATCACCGA TGGAACCAAA	2400
	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAN	2435

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 805 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

10 ATGAAACTTA AGAATTGAAT TGGAAAGACT TCTCAAAGAG AATTGTATGT AACGATGTTG 60
TATTGATTTT TAAGAAAGTA ATTTAATTTG TAAAACTTCT GCTCGTTTAC ACTGCACATT 120
15 GAATACAGGT AACTAATTGG AAGGAGAGGG GAGGTCAC TC TTTGATGGT GGCCCTGAAC 180
CTCATCTCGG TTCCCTGCTG CGCTGCTTGG TGTGACCCAC GGAGGATCCA CTCCCAGGAT 240
GACGTGCTCC GTAGCTCTGC TGCTGATACT GGGTCTGCGA TGCAGCGGCG TGAGGCCTGG 300
20 GCTGGTTGGA GAAGGTCACA ACCCTTCTCT GTTGGTCTGC CTTCTGCTGA AAGACTCGAG 360
AACCAACCAG GGAAGCTGTC CTGGAGGTCC CTGGTCGGAG AGGGACATAG AATCTGTGAC 420
25 CTCTGACAAC TGTGAAGCCA CCTGGGGCTA CAGAAACCAC AGTCTTCCCA GCAATTATTA 480
CAATCTCTGA ATTCCTTGGG GATTTTCTAC TGCCCTTTCA AAGCACTTAA GTGTTAGATC 540
TAACGTGTTT CAGTGTCTGT CTGAGGTGAC TTAAAAATC AGAACAAAAC TTCTATTATC 600
30 CAGAGTCATG GGAGAGTACA CCTTTTCCAG GAATAATGTT TTGGGAAACA CTGAAATGAA 660
ATCTTCCAG TATTATAAAT TGTGTATTTA AAAAAAGAA ACTTTTCTGA ATGCCTACTG 720
35 GCGGTGTATA CCAGGCAGTG TGCCAGTTTA AAAAGATGAA AAAGAATAAA AACTTTTGAG 780
GAACAAAAAA AAAAAAAAAA AAATT 805

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(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGCACGAGAG GCGCCAGTCG CAGGTGTGCT GCTGAGGCGT GAGAATGGCG TCCCGCGGCC 60
GGCGTCCGGA GCATGGCGGA CCCCAGAGC TGTTTTATGA CGAGACAGAA GCCCGGAAAT 120
55 ACGTTCCCAA CTCACGGATG ATTGATATCC AGACCAGGAT GGCTGGCGA GCATTGGAGC 180
TTCTTTATCT GCCAGAGAAT AAGCCCTGTT ACCTGCTGGA TATTGGCTGT GGCCTGGGC 240
60 TGAGTGAAG TTATCTGTCA GATGAAGGC ACTATTGGGT GGCCTGGAT ATCAGCCCTG 300

CCATGCTGGA TGAGGCTGTG GACCGAGAGA TAGAGGGAGA CCTGCTGCTG GGGGATATGG 360
 GCCAGGGCAT CCCATTCAAG CCAGGCACAT TTGATGGTTG CATCAGCATT TCTGCTGTGC 420
 5 AGTGGCTCTG TAATGCTAAC AAGAAGTCTG AAAACCCCTG CAAGCGCCTG TACTGCTTTT 480
 TTGCTTCTCT TTTTCTGTGTT CTCGTCCGGG GATCCCAGAGC TGTCCCTGCAG CTGTACCCTG 540
 10 AGAACTCAGA GCAGTTGGAG CTGATCACAA CCCAGGCCAC AAAGGCAGGC TTCTCCGGTG 600
 GCATGGTGGT AGACTACCCT AACAGTGCCA AAGCAAAGAA ATTCTACCTC TGCTTGTTTT 660
 CTGGGCCTTC GACCTTTATA CCAGAGGGGC TGAGTGAAAA TCAGGATGAA GTTGAACCCA 720
 15 GGGAGTCTGT GTTCACCAAT GAGAGGTTC CATTAAAGGAT GTCGAGGCGG GGAATGGTGA 780
 GGAAGAGTCG GGCATGGGTG CTGGAGAAGA AGGAGCGGCA CAGGCGCCAG GGCAGGGAAG 840
 20 TCAGACCTGA CACCCAGTAC ACCGGCCGCA AGCGCAAGCC CCGCTTCTAA GTCACCACGC 900
 GGTCTGGAA AGGCACCTGC CTCTGCACCTT TTCTATATTG TTCAGCTGAC AAAGTAGTAT 960
 TTTAGAAAAG TTCTAAAGTT ATAAAAATGT TTTCTGCAGT AAAAAAAAAG TTCTCTGGGC 1020
 25 CGGGCGTGGT GGCTCACANC TGTAATCCCA GCACCTTGGG AGGCTGAGGT GGGAGGATCA 1080
 TTTGAGGCCA GGAGTTTGAG ACCTGCCTGG GCAACATAAT GAAACTTCCT TTCCAGGGAG 1140
 30 AAAAAAAAAA AAAAAAAAAA ACTCGA 1166

35 (2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

45 AGAGCGGACG AAGCTGGATA ACAGGGGACC GATGATGTGG CGACCATCAG TTCTGCTGCT 60
 TCTGTTGCTA CTGAGGCACG GGGCCAGGG GAAGCCATCC CCAGACGCAG GCCCTCATGG 120
 CCAGGGGAGG GTGCACCAGG CGGCCCCCTT GAGCGACGCT CCCCATGATG ACGCCACGG 180
 50 GAACTTCCAG TACGACCATG AGGCTTTCCT GGGACGGGAA GTGGCCAAGG AATTGACCA 240
 ACTACCCCA GAGGAAAGCC AGGCCCGTCT GGGGCGGATC GTGACCGCA TGGACCGCGC 300
 55 GGGGACGCGC GACGGCTGGG TGTGCTGGC CGAGCTTCGC GCGTGGATCG CGCACAGCA 360
 GCAGCGGCAC ATACGGGACT CGGTGAGCGC GGCCTGGGAC ACGTACGACA CGGACCGCA 420
 CGGGCGTGTG GGTGGGAGG AGCTGCGCAA CGYACCTAT GGCCACTASG SGCCCGKTGA 480
 60

260

AGAATTTTCAT GACGTGGAGG ATGCAGAGAC YTACAAAAG ATGCTGGYTC GGGACGAGCG 540

GGCTTTCCCG GTGGCCGACC AGGATGGGA CTCGATGGCC ACTCGA 586

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(2) INFORMATION FOR SEQ ID NO: 111:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1134 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

ACCCATTGAG CAGAAGGAGG CCAGGTGGGA AAGCTCCTGG GAAGAGCAGC CAGACTGGAC 60

20 ACTGGGCTGC TTGAGTCCTG AGTCACAATT CAGAATTCCT GGGCTCCCTG GGTGCATTCT 120

ATCATTCCAG TTGAAAGTTT GCTTCCTTCC AGTCATGTGG CTCTTCATTC TACTCTCCTT 180

25 GGCTCTCATT TCAGATGCCA TGTCATGGA TGAAAAGGTC AAGAGAAGTT TGTGCTGGAC 240

ACGGCTTCTG CCATCTGCAA CTACAATGCC CAYTACAAGA ATCACCCCAA ATACTGGTGC 300

CGAGGYTATT TCCGTGAYTA CTGCAACATC ATCGCCTTCT CCCCTAACAG CACCAATCAT 360

30 GTGGCCCTGA AGGACACAGG GAACAGCTC ATTGTCACTA TGTCTGCCT GAACAAANAA 420

GACACGGGCT GGTACTGGTG TGGCATCCAR CGGGACTTTG CMAGGGATGA CATGGATTTT 480

35 ACAGAGCTGA TTGTAAGTGA CGACAAAGGA ACCCTGGCCA ATGACTTTTG GTCTGGGAAA 540

GACCTATCAG GCAACAAAC CAGAAGCTGC AAGGCTCCCA AAGTTGTCCG CAAGCTGACC 600

GCTCCAGGAC GTCCATTCTC ATCATTTGCA TACTGATCAC GGGTTTGGGA ATCATCTCTG 660

40 TAATCAGTCA TTTGACCAA AGGAGGAGAA GTCAAAGGAA TAGAAGGGTA GGCAACACTT 720

TGAAGCCCTT CTCGCGTGTC CTGACTCAA AGGAAATGGC TCCTACTGAA CAGATGTGAC 780

45 TGAAGWTTTT TTTAATTTAG TTNCATAAAG TGATGNCTAC AACAGAWTAA TCACCCATGA 840

CAACTGGCCC CACACCTCAG AGACTGATTC TGATCTCCCA GGAATTCTGA AGGACCCTCT 900

ATCCTTGACA ACAATCATTT GCAGCCAGGT AGCAACGGCR GTAGTCAGAG GAGCTATGAT 960

50 AGACCACACC CAAGCAAGGC TGCCCTCAA TAACATCTCA AGATCTTAGT TCTTATGCAT 1020

TCCATCAGTC AGAAGTGAAG AAGAGGTGGA GAATCTKGAT TGGGGACCAG GAAATCACTT 1080

55 GTATTTTGTT AGCCAATAAA TTCCTAGCCA GTGTTGAATG AAAAAAAAAA AAAA 1134

(2) INFORMATION FOR SEQ ID NO: 112:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

10 CACTTTAAAG CTCTGCTGAG GGAGTTCGGA GCCCAGGCTT TCAGGCGACC TCTGCCCTCC 60
 CTGCCTCTCC TCACCCCTCCC TCTCTTCTTG CAGGGCCTGG GAAGGGCTTT GAGGGAGCCT 120
 GGGAGCCATG TGAAGAGGGG CACGCCTGGG CTGTCCACACA GTTTAGATCC AGTTGGAGGT 180
 15 TCTCCCTGGC TCCTGCAGGC CTGCGGGGAT CTCTCCCCAC TTCAGGCCTC CGGCAGCTGC 240
 CTGCCCTCTT GTCTGTGCTT CAGCCCTGCA CAAAAGCAGC TTGGTGACAC CACTCAGCCA 300
 CCCAGAGTAC GTGTTTACAG GCTTTCAGG TCACCTTCCT GTGGGGTGAA CGTAATGAGG 360
 20 CGGGGCTGGT CCTTGGAATT TCCCTGGGAA AATGGTAACA GACTCCATCC TTGACCCGGG 420
 GATGAGCATG AAGGCATTGT CCCAAAGGCA GAGGCCACCG TGGTAGGAAT TCCACCAAGG 480
 25 CCAGAAGGGA AAAAGGAAGA ACCCACCCTG TCTGGCTGTG CGGGCCCTGG GGAGGGTCGT 540
 GAGTGCAGCC CCTCTCTACT TCYGTGCCTT TGTAACACGT GTAGATAACC GCAGTGGTTG 600
 GCTGAGCCAA GAACTCTCCT AAATCAGTGG CTTTCTCCCC ACCCCTTGCT GGGGAGTCAT 660
 30 TTTTAAAAAA ATCTGTGGGA TATAAAATTG GCCTCCTGCT GCTTCAGCCT ACCTCTCCCT 720
 CTGCTGACTT AATGTCGTGA TTCTGTTTCT TCAGATAATT AAGGCTGTTA GGTGTGTGA 780
 35 GCCTTGAAGT GTGTGTGTGT GTCCAGCGA CTGTCCACTG TCCAGGAGAT GCATGTCTTT 840
 GTATTGGAGA TATTTCTGTA ACTCATCTC TTGGTGCTCA CGATTGCCAT GGCCATAGGG 900
 CCACAGTGCC GTATCTGCTG CAGACATGAT TGTTCCTTGT TCTAGAGGTT TTCTTGTTTT 960
 40 CGAATCTTGC CTGATGAATC CAGCCAGACC AAGGGGCCTA GATTTGACCT CTGTCTGGG 1020
 CTCTGGGCC AGGTGCAGGA ACATCTGAGG CCACTCTGCT GGCCACCTCC AGTGGGTGCT 1080
 45 GACCACAGGA TGGGCTTTGT TTACACTCAT TTTCACCTG ATTCCTGCCC CCACMTTCAT 1140
 AAAAGAACT TCAAAATGCT GACGCTTTGG AGAGTAAGAA AATCAATCTT GGCTGGGCAC 1200
 GGTGGCTCCT GCCTGTGATC CTAGCACTTT GGGAGGCTGA AGCTGAAGGA TCACTTGAGC 1260
 50 TCAGGAGTTG GAGACCAACC CTGGCAACAT AACAGACCC TGTCTCTACA AAAAAAAAAA 1320
 AAAAAAACT CGA 1333

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(2) INFORMATION FOR SEQ ID NO: 113:

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(i) SEQUENCE CHARACTERISTICS:

262

- (A) LENGTH: 1015 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

	GGCACGAGCG GCACGAGCGG CACGAGGTGA CTTCAAGTGT CGGATCTTTT CAGCCTACAT	60
10	CAAGGAGGTG GAGGAACGGC CGGCACCCAC CCCGTGGGCT CCAAGATGCC CTTTGGGGAA	120
	CTGATGTTTCG AATCCAGCAG TAGCTGCGGC TGGGTACATG GCGTCTGTTC CTCAGCCAGC	180
	GGGAGCCGCG TGGCCTGGGT AAGCCACGAC AGCACCGTCT GCCTGGCTGA TGCCGACAAG	240
15	AAGATGGCCG TCGCGACTCT GGCCTCTGAA ACACTACCAC TGCTGGCGCT GACCTTCATC	300
	ACAGACAACA GCCTGGTGGC AGCGGGCCAC GACTGCTTCC CGGTGCTGTT CACCTATGAC	360
20	GCCGCCGCGG GGATGCTGAG CTTCCGCGGG CGGCTGGACG TTCCTAAGCA GAGCTCGCAG	420
	CGTGGCTTGA CGGCCCGGA GCGCTTCCAG AACCTGGACA AGAAGGCGAG CTCCGAGGGT	480
	GGCACGGCTG CGGCGCGGG CCTAGACTCG CTGCACAAGA ACAGCGTCAG CCAGATCTCG	540
25	GTGCTCAGCG GCGCAAGGC CAAGTGCTCG CAGTCTGCA CCACTGGCAT GGATGGCGGC	600
	ATGAGTATCT GGGATGTGAA GAGCTTGAG TCAGCCTGA AGGACCTCAA GATCAAATGA	660
30	CCTGTGAGGA ATATGTTGCC TTCATCCTAG CTGCTGGGA AGCGGGAGA GGGGTGAGG	720
	AGGCTAATGG TTGCTTTGCT GAATGTTTCT GGGGTACCA TACGAGTTCC CATAGGGGCT	780
	GCTCCCTCAA AAAGGGAGGG GACAGATGGG GAGCTTTTCT TACCTATTCA AGGAATACGT	840
35	GCCTTTTCT TAAATGCTTT CATTTATTGA AAAAAAAAAA AAATGCCCCC AAAGCACTAT	900
	GCTGGTCATG AACTGCTTCA AAATGTGGAG GTAATAAAAT GCAACTGTGT AAAAAAAAAA	960
40	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACNC	1015

45 (2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1076 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

55	GGCAGGAGGG GAAAGCCATG CTCCAGGAC TCCTTCCTTG CAGCCTTAAA TCGGTCTGTA	60
	CGGAAAATTC CGCCCTTAG AAACCCACGC TTGGGTGTAA CTTATTATTG TTCTTCCTGA	120
60	CCTACTTCCT GTTATCACT TCCGGGTCA TCATTTTGGC ATTTCCGTGA TCGGGTTGGA	180

ACTATTGAAG CCCGCTTTCA GGTCTTTTC CCCATTTTCC CTTTGAAAGG AAGACTTCTG 240
 GCTTCTCCTA AATCTCCGT CTCTGGGTAA GGGGAGTCCA AGCCTCTGTC ATGAGGAACG 300
 5 GAAATGCGAG GGCCTCGGT GTTACTCTAA AATCCGCCCT CAGCTTGCAC GCCGGAAGCT 360
 GCGATTCTCTG CAGCGGAAGA GCGTGATCT GGCCTTCGAC TCGCTATGTC CACTAACAAT 420
 10 ATGTGCGACC CACGGAGGCC GAACAAAGTG CTGAGGTACA AGCCCCGCC GAGCGAATGT 480
 AACCCGGCCT TGGACGACCC GACGCCGAC TACATGAACC TGTGGGCAT GATCTTCAGC 540
 ATGTGCGGCC TCATGCTTAA GCTGAAGTGG TGTGCTTGGG TCGCTGTCTA CTGCTCCTTC 600
 15 ATCAGCTTTG CCAACTCTCG GAGCTCGGAG GACACGAAGC AAATGATGAG TAGCTTCATG 660
 CTGTCCATCT CTGCCGTGGT GATGTCCTAT CTGCAGAATC CTCAGCCCAT GACGCCCCCA 720
 TGGTGATACC AGCCTAGAAG GGTACATTT TGGACCCTGT CTATCCACTA GGCCTGGGCT 780
 20 TTGGCTGCTA AACCTGCTGC CTTGAGCTGC CATCTGGAC TTCCCTGAAT GAGGCCGTCT 840
 CGGTGCCCC AGCTGGATAG AGGGAACCTG GCCCTTTCCT AGGGAACACC CTAGGCTTAC 900
 25 CCCTCTGCC TCCCTTCCCC TGCCTGCTGC TGGGGGAGAT GCTGTCCATG TTTCTAGGGG 960
 TATTCAATTG CTTTCTCGTT GAAACCTGTT GTTAATAAAG TTTTTCATC TGAAAAAANA 1020
 30 AAAAAAANA RAAAAACNCGN GGGGGGGCCC GGAACCCAAT TCSCCGGATA GTGAGT 1076

35 (2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

45 CCGCTGCTGA TAACTATGGC ATCCCCCGG CCTGCAGGAA TTCGGCACGG AGCTACGGCG 60
 CCGCCTGGCT CTGCTGNCA CCTGCAGGCT CGTCGCGGT GGAGCCCACC CAAGACATCA 120
 GCATCAGCGA CCAGCTGGG GGCAGGACG TGCCCGTGTT CCGGAACCTG TCCCTGCTGG 180
 50 TGGTGGGTGT CGGCGCCGTG TTCTCACTGC TATTCCACCT GGGCACCCGG GAGAGGCGCC 240
 GGCCGCATGC GGAGAGCCA GGCAGCACA CCCCCGTGT GGCCTGTC ACCGCCAGC 300
 CCCTGCTGCT CTGGAAGCAC TGGCTCCGG AGCGGGCTTT CTACCAGGTG GGCATACTGT 360
 55 ACATGACCAC CAGGCTCATC GTGAACCTGT CCCAGACCTA CATGCCCATG TACCTCACCT 420
 ACTCGCTCCA CCTGCCAAG AAGTTCATCG CGACCATTC CCTGGTGATG TACCTCAGCG 480
 60 GCTTCTGTG CTCCTTCTC ATGAAGCCA TCAACAAGTG CATTGGGAGG AACATGACCT 540

	ACTTCTCAGG CCTCCTGGTG ATCCTGGCCT TTGCCGCCCTG GGTGGCGCTG GCGGAGGGAC	600
5	TGGGTGTGGC CGTGTACGCA GCGGCTGTGC TGCTGGGTGC TGGCTGTGCC ACCATCCTCG	660
	TCACCTCGCT GGCCATGACG GCCGACCTCA TCGGTCCCCA CACGAACAGC GGAGCKTTTCG	720
	TGTACGGCTC CATGAGCTTC TTGGATAAGG TGGCCAATGG GCTGGCAGTC ATGGCCATCC	780
10	AGAGCCTGCA CCCTTGCCCC TCAGAGCTCT GCTGCAGGGC CTGCGTGAGC TTTTACCACT	840
	GGGCGATGGT GGCTGTGACG GCGGCGTGG GCGTGGCCGC TGCCCTGTGT CTCTGTAGCC	900
15	TCCTGCTGTG GCCGACCCGC CTGCGACGCT GATGAGACCT GCACGCANTG GCTCACAGCA	960
	GCACGATTTG TGACAGCCCG AGGCGGAGAA CACCGAACAC CCAGTGAAGG TGAGGGGATC	1020
	AGCACGGCGC GGCCACCCAC GCACCCACGC GCTGGAATGA GACTCAGCCA CAAGGAGGTG	1080
20	CGAAGCTCTG ACCCAGGCCA CAGTGCGGAT GCACCTTGAG GATGTCACGC TCAGTGAGAG	1140
	ACACCAGACA CAGAAGGGTA CGCTGTGATC CCACTTCTAT GAAATGTCCA GGACAGACCA	1200
25	ATCCACAGAA TCAGGGAGAG GATTGCTGGG TGCCGGGACT GGGGAGGGG ACCTGGGGGT	1260
	GACTAGGTGA CATAATGGGG ACAGGGCTGC CTTCTGGGTG ATGAGAAATG TCTGGAATCA	1320
	GATGGGATGG CTGCACGGCG TGGTGAAGGT ACTGAACGCC ACCTCACTGT AAGACGGTAG	1380
30	ATTTTGTATT TTACCACAAT AAACAAAACA AAACAAAACC AAAAAAAAAA AAAAAAAAAA	1440
	AAAAAAAAAG AATTCGATAT CAAGCTTATC GATACCGTCG ACCTCGA	1487

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(2) INFORMATION FOR SEQ ID NO: 116:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

	GGCACGAGTG CGCANGCGTG GGGCTCTCTC CTTGTCACTC GGCGCCCGCT GCGGGCTGGT	60
50	GGCTCTGTGG CAGCGGCGGC GGCAGGACTC CGGCACTATG AGCGGCTTCA GCACCGAGGA	120
	GCGCGCCGCG CCTTCTCCCT GGAGTACCGA GTCTTCCTCA AAAATGAGAA AGGACAATAT	180
	ATATCTCCAT TTCATGATAT TCCAATTTAT GCAGATAAGG ATGTGTTTCA CATGGTAGTT	240
55	GAAGTACCAC GCTGGTCTAA TGCAAAAATG GAGATTGCTA CAAAGGACCC TTAAACCCT	300
	ATTAAACAAG ATGTGAAAAA AGGAAAACTT CGCTATGTTG CGAATTGTT CCCGTATAAA	360
60	GGATATATCT GGAACATATG TGCCATCCCT CAGACTTGGG AAGACCCAGG GCACATGAT	420

265

AAACATACTG GCTGTTGTGG TGACAATGAC CCAATTGATG TGTGTGAAAT TGGAAGCAAG 480
 GTATGTGCAA GAGGTGAAAT AATTGGCGTG AAAGTTCTAG GCATATTGGC TATGATTGAC 540
 5 GAAGGGGAAA CCGACTGGAA AGTCATTGCC ATTAATGTGG ATGATCCTGA TGCAGCCAAT 600
 TATAATGATA TCAATGATGT CAAACGGCTG AAACCTGGCT ACTTAGAAGC TACTGTGGAC 660
 TGGTTTAGAA GGTATAAGGT TCCTGATGGA AAACCAGAAA ATGAGTTTGC GTTTAATGCA 720
 10 GAATTTAAAG ATAAGGACTT TGCCATTGAT ATTATTAAAA GCACTCATGA CCATTGGAAA 780
 GCATTAGTGA CTAAGAAAAC GAATGGAAAA GGAATCAGTT GCATGAATAC AACTTTGTCT 840
 15 GAGAGCCCCT TCAAGTGTGA TCCTGATGCT GCCAGAGCCA TTGTGGATGC TTTACCACCA 900
 CCCTGTGAAT CTGCCTGCAC AGTACCAACA GACGTGGATA AGTGGTTCCA TCACCAGAAA 960
 AACTAATGAG ATTCTCTGCG AATACAAGCT GATATTGCTA CATCGTGTTC ATCTGGATGT 1020
 20 ATTAGAAGTA AAAGTAGTAG CTTTTCAAAG CTTTAAATTT GTAGAACTCA TCTAACTAAA 1080
 GTAAATTCTG CTGTGACTAA TCCAATATAC TCAGAATGTT ATCCATCTAA AGCAITTTTC 1140
 25 ATATCTCAAC TAAGATAACT TTTAGCACAT GCTTAAATAT CAAAGCAGTT GTCATTGGGA 1200
 AGTCACTTGT GAATAGATGT GCAAGGGGAG CACATATTGG ATGTATATGT TACCATATGT 1260
 TAGGAAATAA AATTATTTTG CTGAAAAAAA AAAAAAAAAA ACCTSGGGGG GGGSCCGGT 1320
 30 CCCCATTGG CCCTTTGGGG GGNGGTTTAA 1350

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(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2527 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

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CTCTTGCTAC CTTCCTGGCG CAGAGAACCC CGGCTGCTCA GCGCGCTCCG GGGTCATGGA 60
 GATCCCCGGG AGCCTGTGCA AGAAAGTCAA GCTGAGCAAT AACGCGCAGA ACTGGGGAAT 120
 50 GCAGAGAGCA ACCAATGTCA CCTACCAAGC CCATCATGTC AGCAGGAACA AGAGAGGTCA 180
 GGTGGTGGGG ACCAGAGGTG GCTTTCGTGG TTGCACAGTT TGGCTAACAG GCTTGTCTGG 240
 AGCGGGAAAG ACTACTGTGA GCATGGCCTT GGAGGAGTAC CTGGTTTGTC ATGGTATTCC 300
 55 ATGCTACACT CTGGATGGTG ACAATATTCG TCAAGGTCTC AATAAAAAATC TTGGCTTTAG 360
 TCCTGAAGAC AGAGAAGAGA ATGTTTCGACG CATCGCAGAA GTTGCTAAAC TGTTTGCAGA 420
 60 TGCTGGCTTA GTGTGCATCA CRAAGTTTCAT ATCACCTTAC ACTCAGGATC GCAACAATGC 480

	AAGGCAAATT CATGAAGGTG CAAGTTTACC GTTTTTTGAA GTATTTGTTG ATGCTCCTCT	540
5	GCATGTTTGT GAACAGAGGG ATGTCAAAGG ACTCTACAAA AAAGCCCGGG CAGGAGAAAT	600
	TAAAGGTTTC ACTGGGATCG ATTCTGAATA TGAAAAGCCA GAGGCCCTG AGTTGGTGCT	660
	GAAAACAGAC TCCTGTGATG TAAATGACTG TGTCCAGCAA GTGTGGAAC TTCTACAGGA	720
10	ACGGGATATT GTACCTGTGG ATGCATCTTA TGAAGTAAAA GAACTATATG TGCCAGAAAA	780
	TAAACTTCAT TTGGCAAAAA CAGATCGGA AACATTACCA GCACTGAAAA TTAATAAAGT	840
15	GGATATGCAG TGGGTGCAGG TTTTGGCAGA AGGTTGGGCA ACCCCATTGA ATGGCTTTAT	900
	GAGAGAGAGG GAGTACTTGC AGTGCCTTCA TTTTGATTGT CTTCTGGATG GAGGTGTCAT	960
	TAAC TTGTCA GTACCTATAG TTCTGACTGC GACTCATGAA GATAAAGAGA GGCTGGACGG	1020
20	CTGTACAGCA TTTGCTCTGA TGTATGAGGG CCGCCGTGTG GCCATTCTTC GCAATCCAGA	1080
	GTTTTTTGAG CACAGGAAAG AGGAGCGCTG TGCCAGACAG TGGGGAACGA CATGCAAGAA	1140
25	CCACCCCTAT ATTAAGATGG TGATGGAACA AGGAGATTGG CTGATTGGAG GAGATCTTCA	1200
	AGTCTTGGAT CGAGTTTATT GGAATGATGG TCTTGATCAG TATCGTCTTA CTCCTACTGA	1260
	GCTAAAGCAG AAATTTAAAG ATATGAATGC TGATGCTGTC TTGCAATTTC AACTACGCAA	1320
30	CCCAGTGCAC AATGGACATG CCCTGTTAAT GCAGGATACC CATAAGCAAC TTCTAGAGAG	1380
	GGGCTACCGG CGCCCTGTCC TCCTCCTCCA CCCTCTGGGT GGCTGGACAA AGGATGACGA	1440
35	TGTTCCCTTG ATGTGGCGTA TGAAGCAGCA TGCTGCAGTG TTGGAGGAAG GAGTTCTGAA	1500
	TCCTGAGACG ACAGTGGTGG CCATCTTCCC ATCTCCCATG ATGTATGCTG GACCAACTGA	1560
	GGTCCAGTGG CATTGCAGAG CACGGATGGT TGCAGGAGCC AACTTTTACA TTGTTGGACG	1620
40	AGACCTTGCT GGCATGCCTC ATCCAGAAAC AGGGAAGGAT CTTTATGAGC CAAGTCATGG	1680
	TGCCAAAGTG CTGACGATGG CCCCTGGTTT AATCACTTTG GAAATAGTTC CCTTTCGAGT	1740
45	TGCAGCTTAC AACAAGAAAA AGAAGCGTAT GGACTIONAT GACTCTGAAC ACCATGAAGA	1800
	CTTTGAATTT ATTTCAAGAA CACGAATGCG CAAACTTGCT CGAGAAGGCC AGAAACCACC	1860
	TGAAGGTTTC ATGGCTCCCA AGGCTTGGAC CGTGCTGACA GAATACTACA AATCCTTGGG	1920
50	GAAAGCTTAG GCTGTTAACC CAGTCACTCC ACCTTTGACA CATTACTAGT AACAGAGGG	1980
	GACCACATAG TCTCTGTTGG CATTCTTTG TGGTGTCTGT CTGGACATGC TTCCTAAAAA	2040
55	CAGACCATTT TCCTTAACTT GCATCAGTTT TGGTCTGCCT TATGAGTTCT GTTTTGAACA	2100
	AGTGTAACAC ACTGATGGTT TTAATGTATC TTTTCCACTT ATTATAGTTA TATTCCTACA	2160
	ATACAATTTT AAAATGTGCT TTTTATATTA TATTTATGCT TCTGTGTCAT GATTTTMTCA	2220
60	AGCTGTTATA TTAGTTGTAA CCAGTAGTAT TCACATTAAA TCTTGCTTTT TTTCCCTTA	2280

AAAAAAGAAA AAAATTACCA AACAAATAAC TTGGCTAGAC CTTGTTTGA GGATTTTACA 2340
 AGACCTTTGT AGCGATTAGA TTTTPTTCT ACATTGAAAA TAGAACTGC TTCCTTCTT 2400
 5 CTTCCAGTC AGCTATTGGT CTTCCAGCT GTTATAATCT AAAGTATCT TATGATCTGT 2460
 GTAAGCTCTG AATGAACTTC TTTACTCAAT AAAATTAATT TTTGGCTTC TTAACAAAAA 2520
 10 AAAAAA 2527

15 (2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1098 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

25 CGCATCACAG ACAACCCAGA AGGAAAATGG TTGGGCAGAA CAGCAAGGGG TTCATATGGC 60
 TATATTAAAA CAACTGCTGT AGAGATTNNC TATGATTCTT TGAAACTGAA AAAAGACTCT 120
 CTTGGTGCCC CTTCAAGACC TATTGAAGAT GACCAAGAAG TATATGATGA TGTTCAGAG 180
 30 CAGGATGATA TTAGCAGCCA CAGTCAGAGT GGAAGTGGAG GGATATTCCC TCCACCACCA 240
 GATGATGACA TTTATGATGG GATTGAAGAG GAAGATGCTG ATGATGGTTT CCCTGCTCCT 300
 35 CCTAAACAAT TGGACATGGG AGATGAAGTT TACGATGATG TGGATACCTC TGATTTCCTT 360
 GTTTCATCAG CAGAGATGAG TCAAGGAACT AATGTTGGAA AAGCTAAGAC AGAAGAAAAG 420
 GACCTTAAGA AGCTAAAAAA GCAGRAAAAA GAARAAAAAG ACTTCAGGAA AAAATTAAAA 480
 40 TATGATGGTG AAATTAGAGT CCTATATTCA ACTAAAGTTA CAACTTCCAT AACTTCTAAA 540
 AAGTGGGGAA CCAGAGATCT ACAGGTAAAA CCTGGTGAAT CTCTAGAAGT TATACAAACC 600
 45 ACAGATGACA CAAAAGTTCT CTGCAGAAAT GAAGAAGGGA AATATGGTTA TGTCTTCGG 660
 AGTTACCTAG CGGACAATGA TGGAGAGATC TATGATGATA TTGCTGATGG CTGCATCTAT 720
 GACAATGACT AGCACTCAAC TTTGGTCATT CTGCTGTGTT CATTAGGTGC CAATGTGAAG 780
 50 TCTGGATTTT AATTGGCATG TTATTGGGTA TCMAGAAAAT TAATGCACAR AACCCTTAT 840
 TATCATTTGT TATGAAATCC CAATTATCTT TACAACTGT TTAAGTTTG AACATAGAAA 900
 55 ATAATCTCTC TGCTTAATTG TTATCTCAGA AGACTACATT AGTGAGATGT AAGAATTATT 960
 AAATATCCA TTTCCGCTTT GGCTACAATT ATGAAGAAGT TGAAGGTACT TCTTTTAGAC 1020
 CACCAGTAAA TAATCCTCCT TCAAAAAATA AAAATAAAAA AAAAAAATAA AACTCGAGG 1080
 60

GGGGGCCCGG TACCCAAT

1098

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(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1679 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TCGACCCACG CGTCCGGCGA GATCCCTACC GCAGTAGCCG CCTCTGCCGC CGCGGAGCTT	60
CCCGAACCTC TTCAGCCGCC CGGAGCCGCT CCCGGAGCCC GGCCGTAGAG GCTGCAATCG	120
20 CAGCCGGGAG CCCGCAGCCC GCGCCCGAG CCCGCCGCC CCCTTCGAGG GCGCCCCAGG	180
CCGCGCCATG GTGAAGGTGA CGTTCAACTC CGCTCTGGCC CAGAAGGAGG CCAAGAAGGA	240
CGAGCCCCAAG AGCGGCGAGG AGGCGCTCAT CATCCCCCCC GACGCCGTCG CGGTGGACTG	300
25 CAAGGACCCA GATGATGTGG TACCAGTTGG CCAAAGAAGA GCCTGGTGTG GTTGCAATGTG	360
CTTTGGACTA GCATTTATGC TTGCAGGTGT TATTCTAGGA GGAGCATACT TGTACAAATA	420
30 TTTTGCACTT CAACCAGATG ACGTGTACTA CTGTGGAATA AAGTACATCA AAGATGATGT	480
CATCTTAAAT GAGCCCTCTG CAGATGCCCC AGCTGCTCTC TACCAGACAA TTGAAGAAAA	540
TATTAAAATC TTTGAAGAAG AAGAAGTTGA ATTTATCAGT GTGCCTGTCC CAGAGTTTGC	600
35 AGATAGTGAT CTGCCAACA TTGTTTATGA CTTTAACAAG AAACCTACAG CCTATTTAGA	660
TCTTAACCTG GATAAGTGCT ATGTGATCCC TCTGAACACT TCCATTGTGA TGCCACCCAG	720
40 AAACCTACTG GAGTTACTTA TTAACATCAA GGCTGGAACC TATTTGCCTC AGTCCTATCT	780
GATTCATGAG CACATGGTGA TTAATGATCG CATTGAAAAC ATTGATCACC TGGGTTTCTT	840
TATTTATCGA CTGTGTCATG ACAAGGAAAC TTACAAACTG CAACGCAGAG AAACATTATA	900
45 AGGTATTTCAG AAACGTGAAG CCAGCAATTG TTTGCAATT CGGCATTTTG AAAACAAATT	960
TGCCGTGGAA ACTTTAATTT GTTCTTGAAC AGTCAAGAAA AACATTATTG AGGAAAATTA	1020
50 ATATCACAGC ATAACCCAC CCTTTACATT TTGTGCAGTG ATTATTTTTT AAAGTCTTCT	1080
TTCATGTAAG TAGCAAACAG GGCTTTACTA TCTTTTCATC TCATTAATTC AATTAAAACC	1140
ATTACCTTAA AATTTTTTTC TTTCGAAGTG TGGTGTCTTT TATATTTGAA TTAGTAACTG	1200
55 TATGAAGTCA TAGATAATAG TACATGTCAC CTTAGGTAGT AGGAAGAATT ACAATTCTTT	1260
TAAATCATTT ATCTGGATTT TTATGTTTTA TTAGCATTTT CAAGAAGACG GATTATCTAG	1320
60 AGAATAATCA TATATATGCA TACGTAAAAA TGGACCACAG TGACTTATTT GTAGTTGTGA	1380

GTTGCCCTGC TACCTAGTIT GITAGTGCAT TTGAGCACAC ATTTTAATTT TCCTCTAATT 1440
 AAAATGTGCA GTATTTTCAG TGTCAAATAT ATTTAACTAT TTAGAGAATG ATTTCCACCT 1500
 5 TTATGTTTTA ATATCCTAGG CATCTGCTGT AATAATATTT TAGAAAATGT TTGGAATTTA 1560
 AGAAATAACT TGTGTTACTA ATTTGTATAA CCCATATCTG TGCAATGGAA TATAAATATC 1620
 10 ACAAAGTTGT TTAAMWAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAN 1679

15 (2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1308 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

25 TTGGCANCNG GGAGAGGGAA AGAGGAGGAA ATGGGGTTTG AGGACCATGG CTTACCTTTC 60
 CTGCCTTTGA CCCATCACAC CCCATTTCTT CCTCTTTCCC TCTCCCCGCT GCCAAAAAAA 120
 AAAAAAAGG AAACGTTTAT CATGAATCAA CAGGGTTTCA GTCCTTATCA AAGAGAGATG 180
 30 TGGAAAGAGC TAAAGAAACC ACCCTTTGTT CCCAACTCCA CTTTACCCAT ATTTTATGCA 240
 ACACAAACAC TGTCTTTTGG GGTCCCTTTC TTACAGATGG ACCTCTTGAG AAGAATTATC 300
 35 GTATTCCACG TTTTGTAGCC TCAGGTTACC AAGATAAATA TATGTATATA TAACCTTTAT 360
 TATTGCTATA TCTTTGTGGA TAATACATTC AGGTGGTGCT GGGTGATTTA TTATAATCTG 420
 AACCTAGGTA TATCCTTTGG TCTTCCACAG TCATGTTGAG GTGGGCTCCC TGGTATGGTA 480
 40 AAAAGCCAGG TATAATGTAA CTTCAACCCA GCCTTTGTAC TAAGCTCTTG ATAGTGGATA 540
 TACTCTTTTA AGTTTGTAGCC CAATATAGGG TAATGGAAAT TTCCTGCCCT CTGGGTTCCC 600
 45 CATTTTFACT ATTAAGAAGA CAGTGATAA TTTAATAATG CCACCAACTC TGGCTTAGTT 660
 AAGTGAGAGT GTGAAGTGTG TGGCAAGAGA GCCTCACACC TCACTAGGTG CAGAGAGCCC 720
 AGGCCTTATG TTAATAATCAT GCACTTGAAA AGCAAACCTT AATCTGCAA GACAGCAGCA 780
 50 AGCATTATAC GGTCTCTTG AATGATCCCT TTGAAATTTT TTTTGTGTTT GTTTGTTTAA 840
 ATCAAGCCTG AGGCTGGTGA ACAGTAGCTA CACACCCATA TTGTGTGTTT TGTGAATGCT 900
 55 AGCTCTCTTG AATTTGGATA TTGGTTATTT TTTATAGAGT GTAAACCAAG TTTTATATTC 960
 TGCAATGCGA ACAGGTACCT ATCTGTTTCT AAATAAACT GTTTACATTC ATTATGGGGT 1020
 ATGTATGACC TTCATTTTCC AAGAAATAGA ACTCTAGCTT AGAATTATGG ATGCTCTAAA 1080
 60

270

ATGTCAGAAT GGGAACTCTC CTCGAAGTTC TCCCAAATC AGAGACAGCA CTGCCCTTCTC 1140
 CTAAATGATT ATTCTTTTCT CCCTGTTTTC TGGTATTTTC TAGGCATCCT TCTCACCACA 1200
 5 GCCATAACCC TTTTCTACTT CCATTAGGCC GTATAACTGG NGGGACNGCT GGTCCGTATA 1260
 TAATACTGGT WCCAACAMAG GGGTCTGGA TGTACACMAG GTTATCTT 1308

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(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

GGCACAGGAG CGACCCGGGA GAAGGAGGGC CAMGAKGCGG AAGCGGAGGA GTCTCCAGGA 60
 GACCCGGGGA CAGCATCGCC CAGGCCCTG TTTGCAGGCC TTTCAGATAT ATCCATCTCA 120
 25 CAAGACATCC CCGTAGAAGG AGAAATCACC ATTCCTATGA GATCTCGCAT CCGGGAGTTT 180
 GACAGCTCCA CATTAAATGA ATCTGTTGCG AATACCATCA TCGGTGATCT AAAAGCTGTT 240
 30 GGGAAAAAAT TCATGCATGT TTTGTACCCA AGGAAAAGTA ATACTCTTTT GAGAGATTGG 300
 GATTTGTGGG GCCCTTTGAT CCTTTGTGTG ACACTCGCAT TAATGCTGCA AAGAGACTCT 360
 GCAGATAGTG AAAAAGATGG AGGGCCCCAA TTTGCAGAGG TGTTTGTCAT TGTCTGGTTT 420
 35 GGTGCAGTTA CCATCACCCCT CAACTCAAAA CTCTTGGAG GGAACATATC TTTTTCAG 480
 AGCCTCTGTG TGCTGGGTTA CTGTATACTT CCCTTGACAG TAGCAATGCT GATTTGCCCG 540
 40 CTGGTACTTT TGGCTGATCC AGGACCTGTA AACTTCATGG TTCGGCTTTT TGTGGTGATT 600
 GTGATGTTTG CCTGGTCTAT AGTTGCCTCC ACAGCTTTCC TTGCTGATAG CCAGCCTCCA 660
 AACCGCAGAG CCCTAGCTGT TTATCCTGTT TTCCTGTTT ACTTTGTCAT CAGTTGGATG 720
 45 ATTCTCACCT TTAATCCTCA GTAAATCAGG AATGGGAAAT TAAAAACCAG TGAATTGAAA 780
 GCACATCTGA AAGATGCAAT TCACCATGGA GCTTGTCTC TGGCCCTTAT TTGTCTAATT 840
 50 TTGGAGGTAT TTGATAACTG AGTAGGTGAG GAGATTAAAA GGGAGCCATA TAGCACTGTC 900
 ACCCCTTATT TGAGGAACTG ATGTTTGAAA GGCTGTTCTT TTCTCTCTTA ATGTCATTTC 960
 55 TTTAAAAATA CATGTGCATA CTACACACAG TATATAATGC CTCCTTAAGG CATGATGGAG 1020
 TCACCGTGGT CCATTTGGGT GACAACCAGT GACTTGGGAA GCACATAGAT ACATCTTACA 1080
 AGTTGAATAG AGTTGATAAC TATTTTCAGT TTTGAGAATA CCAGTTCAGG TGCAGCTCTT 1140
 60 AAACACATTG CCTATGACT ATTAGAATAT GCCTCTCTTT TCATAAATAA AAATACATGG 1200

TCTATATCCA TTTTCTTTTA TTTCTCTCTC TTAAGCTTAA AAAGGCAATG AGAGAGGTTA 1260
 GGAGTGGGTT CATAACCGGA GAATGAGAAA ACATGCATTA ACCAATATTC AGATTTTGAT 1320
 5 CAGGGGAAAT TCTAYACTTG TTGCAAAAAA AAAAAAAAAA AAACCTCGAGG GGGGCCCGGT 1380
 ACCCAATCGC NGTATATGAT CGNAAACAAT C 1411

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(2) INFORMATION FOR SEQ ID NO: 122:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GCTTTGGCTT TTTTGGCGG ACTGGGGCGC CCTCCGAAG CGTTTCCAAC TTTCCAGAAG 60
 25 TTTCTCGGGA CGGGCAGGAG GGGGTGGGGA CTGCCATATA TAGATCCCGG GAGCAGGGGA 120
 GCGGGCTAAG AGTAGAATCG TGTGCGGGCT CGAGAGCGAG AGTCACGTCC CGGCGCTAGC 180
 CAGCCCGACC CAGGCCACC GTGGTGCACG CAAACCACTT CCTGGCCATG CGCTCCCTCC 240
 30 TGCTTCTCAG CGCCTTCTGC CTCCTGGAGG CGGCCCTGGC CGCCGAGGTG AAGAAACCTG 300
 CAGCCGCAGC AGCTCCTGGC ACTGCGGAGA AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG 360
 35 AGCGCANGCC GGCTGGCCT TCAGCTGTGA CCAGGCCATG GCCAAGGACC AGGCAGTGGA 420
 GAACATCCTG GTGTACCCG TGGTGGTGGC CTCGTGCTG GGGCTCGTGT CGCTGGGCGG 480
 CAAGGCGACC ACGGCGTCGC AGGCCAAGGC AGTCTGAGC GCCGAGCAGC TGCAGCAGCA 540
 40 GGAGGTGCAC GCCGGCCTGG GCGAGCTGCT GCGCTCACTC AGCAACTCGA CGGCGCGCAA 600
 CGTGACCTGG AAGCTGGGCA GCCGACTGTA CGGACCCAGC TCAGTGAGCT TCGCTGATGA 660
 45 CTTCGTGCGC ACAGCAAGCA GCACTACAAC TGCAGCACT CCAAGATCAA CTTCGCGGAC 720
 AAGCGCAGNG CGCTGCAGTC CATCAACGAG TGGGCCGCGC AGACCACCGA CGGCAAGCTG 780
 CCCGAGGTCA CCAAGGACGT GGAGCGCACG GACGGCGCCC TGCTAGTCAA CGCCATGTTT 840
 50 TTCAAGCCAC ACTGGGATGA GAAATTCCAC CACAAGATGG TGGACAACCG TGGCTTCATG 900
 GTGACTCGGT CCTATACVGT GGGTGTCAATG ATGATGCACC GGACAGGCCT CTACAACTAC 960
 55 TACGACGACG AGAAGGAAAA GCTGCAAAATC GTGGAGATGC CCCTGGCCCA CAAGCTCTCC 1020
 AGCCTCATCA TCCTCATGCC CCATCACGTG GAGCCTCTCG AGCGCCTTGA AAAGCTGCTA 1080
 ACCAAAGAGC AGCTGAAGAT CTGGATGGGG AAGATGCAGA AGAAGGCTGT TGCCATCTCC 1140
 60

TTGCCCAAGG GTGTGGTGGG GGTGACCCAT GACCTGCAGA AACACCTGGC TGGGCTGGGC 1200
 CTGACTGAGG CCATTGACAA GAACAAGGCC GACTTTRTCAC GCATGTCAGG CAAGAAGGAC 1260
 5 CTGTACCTGG CCAGCGTGTT CCACGCCACC GCCTTTGAGT TGGACACAGA TGGCAACCCC 1320
 TTTGACCAGG ACATCTACGG GCGCGAGGAG CTGCGCANCC CAAGCTGTTC TACGCCGACC 1380
 10 ACCCCTTCAT CTTCTTAGTG CGGGACACCC AAAGCGGCTC CTTGCTATTC ATTGGGCGCC 1440
 TGGTCCGCC TAAGGGTGAC AAGATGCGAG ACGAGTTATA GGGCCTCAGG GTGCACACAG 1500
 GATGGCAGGA GGCATCCAAA GGCTCCTGAG ACACATGGGT GCTATTGGGG TTGGGGGGGA 1560
 15 GGTGAGGTAC CAGCCTTGA TACTCCATGG GGTGGGGGTG GAAAARCAGA CCGGGGTTC 1620
 CGTGTGCTG AGCGGACCTT CCCAGCTAGA ATTCACTCCA CTTGGACATG GGCCCCAGAT 1680
 ACCATGATGC TGAGCCCGGA AACTCCACAT CCTGTGGGAC CTGGGCCATA GTCATTCTGC 1740
 20 CTGCCCTGAA AGTCCCAGAT CAAGCCTGCC TCAATCAGTA TTCATATTTA TAGCCAGGTA 1800
 CCTTCTCACC TGTGAGACCA AATTGAGCTA GGGGGGTTCAG CCAGCCCTCT TCTGACACTA 1860
 25 AAACACCTCA GCTGCCTCCC CAGCTCTATC CCAACCTCTC CCAACTATAA AACTAGGTGC 1920
 TGCAGCCCTT GGGACCAGGC ACCCCAGAA TGACCTGGCC GCAGTGAGGC GGATTGAGAA 1980
 GGAGCTCCCA GGAGGGGCTT CTGGCAGAC TCTGGTCAAG AAGCATCGTG TCTGGCGTTG 2040
 30 TGGGGATGAA CTTTTGTGTT TGTTCCTTCC TTTTTTAGTT CTTCAAAGAT AGGGAGGGAA 2100
 GGGGAACAT GAGCCTTTGT TGCTATCAAT CCAAGAACTT ATTTGTACAT TTTTTTTTTC 2160
 35 AATAAACTT TTCCAATGAC AAAAAAAAAA AAAAAAAAAA AAAAAGGGGS GGGCCGCTCC 2220
 TAGAGGGATC CTTCCGANGG NGCCCAATCG AAAATN 2256

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(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 829 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ATGCGCTCCC TCCTGCTTCT CAGCGCTTC TGCTCTCTGG AGGCGGCCCT GGCGCCGAG 60
 GTGAAGAAAC CTGCAGCCGC AGCAGCTCCT GGCAGTCCG AGAAGTTGAG CCCCAGGCG 120
 55 GCCACGCTTG CCGAGCGCAA GCGGCTGGC CTTAGCTTG TACCAGCCA TGGCCAAGGA 180
 CCAGGCAGTG GAGAACATCC TGGTGTACC CGTGGTGGTG GCCTCGTCGC TGGGCTCGT 240
 60 GTCGCTGGG GGAAGGCGA CCACGGCGTC GCAGGCCAAG GCAGTGCTGA GCGCCGAGCA 300

GCTGCGCGAC GAGGAGGTGC ACGCCGGCCT GGGCGAGCTG CTGCGCTCAC TCAGCAACTC 360
 CACGGCGCGC AACGTGACCT GGAAGCTGGG CAGCCGACTG TACGGACCCA GCTCAGTGAG 420
 5 CTTCGCTGAT GACTTCGTGC GCAGCAGCAA GCAGCACTAC AACTGCGAGC ACTCCAAGAT 480
 CAACTTCCGC GACAAGCGCA GCGCGCTGCA GTCCATCAAC GAGTGGGCGG CGCAGACCAC 540
 10 CGACGGCAAG CTGCCCAGG TCACCAAGGA CGTGGAGCGC ACGGACGGCG CCCTGTTAGT 600
 CAACGCCATG TTCTTCAAGC CACACTGGGA TGAGAAATTC CACCACAAGA TGGTGGACAA 660
 CCGTGGCTTC ATGGTGACTC GGTCTATAC CGTGGGTGTC ATGATGATGC ACCGGACAGG 720
 15 CCTCTACAAC TACTACGACG ACGAGAAGGA AAAGCTGCAA ATCGTGGAGA TGCCCTGGC 780
 CCACAAGCTC TCCAGCCTCA TCATCCTCAT GCCCCATCAC GTGGAGCCT 829

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(2) INFORMATION FOR SEQ ID NO: 124:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

CCTCCGGAAG CGTTTCCAAC TTTCCAGAAG TTTCTCGGGA CGGGCAGGAG GGGGTGGGGA 60
 35 CTGCCATATA TAGATCCCGG GAGCAGGGGA GCGGGCTAAG AGTAGAATCG TGTGCGGCT 120
 CGAGAGCGAG AGTCACGTCC CGGCGCTAGC CAGCCCGACC CAGGCCACC GTGGTGACG 180
 CAAACCACTT CTGGCCATG CGCTCCCTCC TGCTTCTCAG CGCTTCTGC CTCCTGGAGG 240
 40 CGGCCCTGGC CGCGAGGTG AAGAAACCTG CAGCCGAGC AGCTCCTGGC ACTGCGGAGA 300
 AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG AGCGCAGNCG GCCTGGCCTT CAGCTTGATC 360
 45 CAGGCCATGG CCAAGGACCA GGCAGTGGAG AACATCCTGG TGTCAACCGT GGTGGTGGCC 420
 TCGTCGCTGG GGCTCGTGTC GCTGGGCGGC AAGGCGACCA CGGCGTGCA GGCCAAGGCA 480
 GTGCTGAGCG CCGAGCAGCT GCGGACGAG GAGGTGCACG CCGGCCTGGG CGAGCTGCTG 540
 50 CGCTCACTCA GCAACTCSAC GGCGGCAAC GTGACCTGGA AGCTGGGCAG CCGACTGTAC 600
 GGACCCAGCT CAGTGAGCTT CGCTGATGAC TTCGTGCGCA CAGCAAGCAG CACTACAAC 660
 55 GCGAGCACTC CAAGATCAAC TTCCGCGACA AGCGCACGCG CTGCAGTCCA TCAACGAGTG 720
 GGCCGCGCAG ACCACCGACG GCAAGCTGCC CGAGGTCACC AAGGACGTGG AGCGCACGGA 780
 CGGCGCCCTG YTAGTCAACG CCATGTTCTT CAAGCCACAC TGGGATGAGA AATTCACCA 840
 60

274

CAAGATGGTG GACAACCGTG GCTTCATGGT GACTCGGTCC TATACYGTGG GTGTCATGAT 900
 GATGCACCGG ACAGGCCTCT ACAACTACTA CGACGACGAG AAGGAAAAGC TGCAAATCGT 960
 5 GGAGATGCCC CTGGCCCACA AGCTCTCCAG CCTCATCATC CTCATGCCCC ATCAGTGGA 1020
 GCCTCTGAG CGCCTTGAAA AGCTGCTAAC CAAAGAGCAG CTGAAGATCT GGATGGGGAA 1080
 10 GATGCAGAAG AAGGCTGTTG CCATCTCCTT GCCCAAGGGT GTGGTGGAGG TGACCCATGA 1140
 CCTGCAGAAA CACCTGGCTG GGCTGGGCCT GACTGAGGCC ATTGACAAGA ACAAGGCCGA 1200
 CTTRTCACGC ATGTCAGGCA AGAAGGACCT GTACCTGGCC AGCGTGTTC ACGCCACCGC 1260
 15 CTTTGAGTTG GACACAGATG GCAACCCCTT TGACCAGGAC ATCTACGGG GCGAGGAGCT 1320
 GCGCASCCCA AGCTGTTCTA CGCCGACCAC CCCTTCATCT TCCTAGTGGG GGACACCCAA 1380
 AGCGGCTCCC TGCTATTCAT TGGGCGCCTG GTCCGGCCTA AGGGTGACAA GATGCGAGAC 1440
 20 GAGTTATAGG GCCTCAGGGT GCACACAGGA TGGCAGGAGG CATCCAAAGG CTCCTGAGAC 1500
 ACATGGGTGC TATTGGGGTT GGGGGGAGG TGAGGTACCA GCCTTGATA CTCCATGGGG 1560
 25 TGGGGGTGGA AAARCAGACC GGGGTTCCTG TGTGCTGAG CGGACCTTC CAGCTAGAAT 1620
 TCACTCCACT TGGACATGGG CCCAGATAC CATGATGCTG AGCCCGGAAA CTCCACATCC 1680
 TGTGGGACCT GGGCCATAGT CATTCTGCCT GCCCTGAAAG TCCCAGATCA AGCCTGCCTC 1740
 30 AATCAGTATT CATATTTATA GCCAGGTACC TTCTCACCTG TGAGACCAA TTGAGCTAGG 1800
 GGGGTCAGCC AGCCCTCTTC TGACACTAAA ACACCTCAGC TGCCTCCCCA GCTCTATCCC 1860
 35 AACCTCTCCC AACTATAAAA CTAGGTGCTG CAGCCCCTGG GACCAGGCAC CCCAGAATG 1920
 ACCTGGCCGC AGTGAGGCGG ATTGAGAAGG AGCTCCAGG AGGGGCTTCT GGGCAGACTC 1980
 TGGTCAAGAA GCATCGTGTG TGGCGTTGTG GGGATGAACT TTTTGTMTTG TTTCTTCCTT 2040
 40 TTTTAGTTCT TCAAAGATAG GGAGGGAAGG GGGAAATGA GCCTTTGTTG CTATCAATCC 2100
 AAGAACTTAT TTGTACATTT TTTTITTCAT TAAAACTTTT CCAATGACAA AAAAAAAAAA 2160
 45 AAAAAAAAAA MMGGGGSGG GCCGCTCCTA GAGGGATCCC TCCGANGNG CCCAATCGAA 2220
 AAT 2223

50

(2) INFORMATION FOR SEQ ID NO: 125:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

60

Met Lys Lys Gln Ser Lys Arg Cys Leu Trp Lys Pro Pro Gly Ser Leu

275

1 5 10 15
 Arg Arg Leu Trp Trp Met Arg Ala Leu Leu Ile Leu Lys Tyr Ile
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 126:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

15

Met Lys Lys Ser Leu Glu Asn Leu Asn Arg Leu Gln Val Met Leu Leu
 1 5 10 15

20

His Leu Thr Ala Ala Phe Leu Gln Arg Ala His Xaa Ile Leu Thr Thr
 20 25 30

Arg Met Ser Leu Gly Phe Gln Ser Pro His Leu Thr Met
 35 40 45

25

(2) INFORMATION FOR SEQ ID NO: 127:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

35

Met His Asn Gln Arg Gln Val Phe Leu Phe His Leu Phe Ser Asn Tyr
 1 5 10 15

40

Leu Leu Ser Ile Asn Ser Val Pro Gly Thr Leu Leu Ala Ala Thr Tyr
 20 25 30

Cys Leu Asn Met Thr Tyr Gly
 35

45

(2) INFORMATION FOR SEQ ID NO: 128:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

55

Met Arg Lys Lys Phe Leu Leu Ala Gln Val Phe Leu Ser Leu Ser Val
 1 5 10 15

Met Pro Ser Met Pro Val Thr
 20

60

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

10 Met Val Leu Leu Cys Leu Leu Leu Val Pro Leu Leu Leu Ser Leu Phe
1 5 10 15

Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln Glu Glu
20 25 30

15 Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu Thr Pro Asn
35 40 45

20 Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp Thr Ile Pro His
50 55 60

Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala Asn Thr Val Tyr Ser
65 70 75 80

25 Thr Val Glu Ile Pro Lys Lys Met Glu Asn Pro His Ser Leu Leu Thr
85 90 95

Met Pro Asp Thr Pro Arg Leu Phe Ala Tyr Glu Asn Val Ile
100 105 110

30

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

40 Met Leu Leu Leu Phe Ile Tyr Phe Tyr Ser His Pro Ala Pro Val Pro
1 5 10 15

Ala Gly Ala Thr Ser Lys Pro Arg Tyr Arg Val Ile Thr Cys Gly Pro
45 20 25 30

Ala Ser Val Phe Ser Thr Ser Phe Ser His Ser Pro Pro Ala Arg Cys
35 40 45

50 Leu Gly Arg Leu Glu Gln Met Phe His Phe Gly Leu Ala Ser Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Met Pro Phe Pro Ile Ser Ile Leu Gln Leu Cys Leu Gln Ile Ser Asn
 1 5 10 15
 5 Leu Ser Phe Cys Leu Gln Lys Ile Tyr Lys Ile Pro Phe Val
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Met Ala Ala Ala Cys Arg Ser Val Lys Gly Leu Val Ala Val Ile Thr
 1 5 10 15
 Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Asp Asp Leu Trp Gly
 20 25 30
 25 Arg Glu Pro Leu Leu Cys Phe Trp Thr Cys Pro Thr Arg Val Gly Arg
 35 40 45
 Pro Lys Pro Arg Ser
 50

30

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

40

Met Leu Leu Val Tyr Asp Leu Tyr Leu Xaa Pro Lys Leu Trp Ala Leu
 1 5 10 15
 Ala Thr Pro Gln Lys Asn Gly Lys Gly Ala Arg Xaa Gly Asp Gly Thr
 20 25 30
 Pro Ala Gln Ala Phe Trp Asp Phe Trp Ser His Leu Ile Ser Ala Asp
 35 40 45

45

50 Pro Gln Thr Trp Glu Arg Ala Ala Pro
 50 55

55 (2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Met Arg Leu Ser Ala Leu Leu Ala Leu Ala Ser Lys Val Thr Leu Pro
 1 5 10 15
 5 Pro His Tyr Arg Tyr Gly Met Ser Pro Pro Gly Ser Val Ala Asp Lys
 20 25 30
 10 Arg Lys Asn Pro Pro Trp Ile Arg Arg Arg Pro Val Val Val Glu Pro
 35 40 45
 Ile Ser Asp Glu Asp Trp Tyr Leu Phe Cys Gly Asp Thr Val Glu Ile
 50 55 60
 15 Leu Glu Gly Lys Asp Ala Gly Lys Gln Gly Lys Val Val Gln Val Ile
 65 70 75 80
 Arg Gln Arg Asn Trp Val Val Val Gly Gly Leu Asn Thr His Tyr Arg
 85 90 95
 20 Tyr Ile Gly Lys Thr Met Asp Tyr Arg Gly Thr Met Ile Pro Ser Glu
 100 105 110
 Ala Pro Leu Leu His Arg Gln Val Lys Leu Val Asp Pro Met Asp Arg
 115 120 125
 25 Lys Pro Thr Glu Ile Glu Trp Arg Phe Thr Glu Ala Gly Glu Arg Val
 130 135 140
 30 Arg Val Ser Thr Arg Ser Gly Arg Ile Ile Pro Lys Pro Glu Phe Pro
 145 150 155 160
 Arg Ala Asp Gly Ile Val Pro Glu Thr Trp Ile Asp Gly Pro Lys Asp
 165 170 175
 35 Thr Ser Val Glu Asp Ala Leu Glu Arg Thr Tyr Val Pro Cys Leu Lys
 180 185 190
 40 Thr Leu Gln Glu Glu Val Met Glu Ala Met Gly Ile Lys Glu Thr Arg
 195 200 205
 Lys Tyr Lys Lys Val Tyr Trp Tyr
 210 215

45

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

55 Met Ser Leu Arg Gln Lys Ser Ser Phe Arg Leu Met Val Met Ser Leu
 1 5 10 15
 Thr Ile Leu Lys Leu Ser Lys Thr Thr Val Leu Cys Leu Arg Cys Leu
 20 25 30

60

His Ser Leu Lys Leu Thr Trp Arg Asp Gly Ala Arg Cys Ile Asn Ala
 35 40 45

Glu

5

(2) INFORMATION FOR SEQ ID NO: 136:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Met Ser Gly Ser Phe Ile Leu Cys Leu Ala Leu Val Thr Arg Trp Ser
 1 5 10 15

20

Pro Gln Ala Ser Ser Val Pro Leu Ala Val Tyr Glu Ser Lys Thr Arg
 20 25 30

Lys Ser Tyr Arg Ser Gln Arg Asp Arg Asp Gly Lys Asp Arg Ser Gln
 35 40 45

25

Gly Met Gly Leu Ser Leu Leu Val Glu Thr Arg Lys Leu Leu Leu Ser
 50 55 60

Ala Asn Gln Gly
 65

30

(2) INFORMATION FOR SEQ ID NO: 137:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Met Cys Phe Arg Phe Phe Leu Phe Cys Ser Arg Ile Leu Leu Lys Leu
 1 5 10 15

45

Phe Phe Leu Leu Phe Pro Ala Ser Ala Phe Pro Leu Ser Thr Arg Ser
 20 25 30

Ser Leu Ser Val Asn Glu His Val Val Val Ser Pro Arg Ser Thr Val
 35 40 45

50

Ser Ile Ser Arg
 50

55

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 541 amino acids

(B) TYPE: amino acid

60

280

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

5	Met Val Arg Thr Asp Gly His Thr Leu Ser Glu Lys Arg Asn Tyr Gln	1	5	10	15
	Val Thr Asn Ser Met Phe Gly Ala Ser Arg Lys Lys Phe Val Glu Gly	20	25	30	
10	Val Asp Ser Asp Tyr His Asp Glu Asn Met Tyr Tyr Ser Gln Ser Ser	35	40	45	
	Met Phe Pro His Arg Ser Glu Lys Asp Met Leu Ala Ser Pro Ser Thr	50	55	60	
15	Ser Gly Gln Leu Ser Gln Phe Gly Ala Ser Leu Tyr Gly Gln Gln Ser	65	70	75	80
	Ala Leu Gly Leu Pro Met Arg Gly Met Ser Asn Asn Thr Pro Gln Leu	85	90	95	
20	Asn Arg Ser Leu Ser Gln Gly Thr Gln Leu Pro Ser His Val Thr Pro	100	105	110	
	Thr Thr Gly Val Pro Thr Met Ser Leu His Thr Pro Pro Ser Pro Ser	115	120	125	
	Arg Gly Ile Leu Pro Met Asn Pro Xaa Asn Met Met Asn His Ser Gln	130	135	140	
30	Val Gly Gln Gly Ile Gly Ile Pro Ser Arg Thr Asn Ser Met Ser Ser	145	150	155	160
	Ser Gly Leu Gly Ser Pro Asn Arg Ser Ser Pro Ser Ile Ile Cys Met	165	170	175	
35	Pro Lys Gln Gln Pro Ser Arg Gln Pro Phe Thr Val Asn Ser Met Ser	180	185	190	
	Gly Phe Gly Met Asn Arg Asn Gln Ala Phe Gly Met Asn Asn Ser Leu	195	200	205	
	Ser Ser Asn Ile Phe Asn Gly Thr Asp Gly Ser Glu Asn Val Thr Gly	210	215	220	
45	Leu Asp Leu Ser Asp Phe Pro Ala Leu Ala Asp Arg Asn Arg Arg Glu	225	230	235	240
	Gly Ser Gly Asn Pro Thr Pro Leu Ile Asn Pro Leu Ala Gly Arg Ala	245	250	255	
50	Pro Tyr Val Gly Met Val Thr Lys Pro Ala Asn Glu Gln Ser Gln Asp	260	265	270	
	Phe Ser Ile His Asn Glu Asp Phe Pro Ala Leu Pro Gly Ser Ser Tyr	275	280	285	
	Lys Asp Pro Thr Ser Ser Asn Asp Asp Ser Lys Ser Asn Leu Asn Thr	290	295	300	
60					

281

Ser Gly Lys Thr Thr Ser Ser Thr Asp Gly Pro Lys Phe Pro Gly Asp
 305 310 315 320
 5 Lys Ser Ser Thr Thr Gln Asn Asn Asn Gln Gln Lys Lys Gly Ile Gln
 325 330 335
 Val Leu Pro Asp Gly Arg Val Thr Asn Ile Pro Gln Gly Met Val Thr
 340 345 350
 10 Asp Gln Phe Gly Met Ile Gly Leu Leu Thr Phe Ile Arg Ala Ala Glu
 355 360 365
 Thr Asp Pro Gly Met Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr
 370 375 380
 15 Leu Gly Leu Asn Leu Asn Ser Pro Glu Asn Leu Tyr Pro Lys Phe Ala
 385 390 395 400
 Ser Pro Trp Ala Ser Ser Pro Cys Arg Pro Gln Asp Ile Asp Phe His
 405 410 415
 20 Val Pro Ser Glu Tyr Leu Thr Asn Ile His Ile Arg Asp Lys Leu Ala
 420 425 430
 25 Ala Ile Lys Leu Gly Arg Tyr Gly Glu Asp Leu Leu Phe Tyr Leu Tyr
 435 440 445
 Tyr Met Asn Gly Gly Asp Val Leu Gln Leu Leu Ala Ala Val Glu Leu
 450 455 460
 30 Phe Asn Arg Asp Trp Arg Tyr His Lys Glu Glu Arg Val Trp Ile Thr
 465 470 475 480
 Arg Ala Pro Gly Met Glu Pro Thr Met Lys Thr Asn Thr Tyr Glu Arg
 485 490 495
 35 Gly Thr Tyr Tyr Phe Phe Asp Cys Leu Asn Trp Arg Lys Val Ala Lys
 500 505 510
 40 Glu Phe His Leu Glu Tyr Asp Lys Leu Glu Glu Arg Pro His Leu Pro
 515 520 525
 Ser Thr Phe Asn Tyr Asn Pro Ala Gln Gln Ala Phe Xaa
 530 535 540
 45

(2) INFORMATION FOR SEQ ID NO: 139:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Met Ile Cys Pro Gln Cys Pro Leu Ser Leu Leu Cys Leu Ile Ser Ser
 1 5 10 15
 60 Leu Cys Ser Leu Val Ile Gln Ile Ser Leu Lys Thr Ile Arg Asp Ile
 20 25 30

Thr Leu Leu Asn Met Val Gly Ile Lys Phe Ser Ile Ser Leu Ser Asn
 35 40 45

5 Lys Ile Asn Ile Asn Ser Arg Thr Trp Xaa
 50 55

10 (2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu Leu
 1 5 10 15
 20 Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu Thr Glu
 20 25 30
 25 Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu
 35 40 45
 Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr
 50 55 60
 30 Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg
 65 70 75 80
 Asp Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu
 85 90 95
 35 Glu Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile
 100 105 110
 40 Ile Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val
 115 120 125
 Pro Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile
 130 135 140
 45 Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu Val
 145 150 155 160
 Gly Met Ala Met Val Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu
 165 170 175
 50 Tyr Arg Lys Ala Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu
 180 185 190
 Glu Lys Arg Asn Lys Ser Lys Lys Lys Xaa
 195 200

60 (2) INFORMATION FOR SEQ ID NO: 141:

283

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser
 1 5 10 15

10 Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys
 20 25 30

Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys
 35 40 45

15 Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala
 50 55 60

20 Ala Trp Thr Val Arg Val Cys Glu Ser Pro Glu Ser Pro Ala Gln Pro
 65 70 75 80

Ser Gly Ser Ser Leu Pro Ala Trp Tyr His Asp Gln Gln Asp Val Thr
 85 90 95

25 Ser Asn Phe Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser
 100 105 110

Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val
 115 120 125

30 Cys Leu Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val
 130 135 140

35 Ala Val Val Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val
 145 150 155 160

His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala
 165 170 175

40 Ala Ala Asn Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys
 180 185 190

Leu Leu Lys Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys
 195 200 205

45 Phe Leu Pro Ser Tyr Pro Pro Val Xaa
 210 215

50

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

60 Met Ser Asn Thr Thr Val Pro Asn Ala Pro Gln Ala Asn Ser Asp Ser
 1 5 10 15

Met Val Gly Tyr Val Leu Gly Pro Phe Phe Leu Ile Thr Leu Val Gly
 20 25 30

5 Val Val Val Ala Val Val Met Tyr Val Gln Lys Lys Lys Arg Val Asp
 35 40 45

Arg Leu Arg His His Leu Leu Pro Met Tyr Ser Tyr Asp Pro Ala Glu
 50 55 60

10 Glu Leu His Glu Ala Glu Gln Glu Leu Leu Ser Asp Met Gly Asp Pro
 65 70 75 80

15 Lys Val Val His Gly Trp Gln Ser Gly Tyr Gln His Lys Arg Met Pro
 85 90 95

Leu Leu Asp Val Lys Thr
 100

20

(2) INFORMATION FOR SEQ ID NO: 143:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

30 Met Arg Glu Cys Gln Glu Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe
 1 5 10 15

Ser Leu Val Ser Met Leu Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr
 20 25 30

35 Leu Ala Ala Asn Ser Arg Phe Gly Ser Leu Pro Lys Val Ala Leu Ala
 35 40 45

40 Gly Leu Leu Gly Phe Gly Leu Gly Lys Val Ser Tyr Ile Gly Val Cys
 50 55 60

Gln Ser Lys Phe His Phe Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe
 65 70 75 80

45 Gly Pro Gln His Asn Arg His Cys Leu Leu Thr Cys Glu Glu Cys Lys
 85 90 95

Ile Lys His Gly Leu Ser Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 100 105 110

50

55

(2) INFORMATION FOR SEQ ID NO: 144:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid

285

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

5 Met Lys Asn Asp Arg Asn Gln Gly Phe Ser Leu Leu Gln Leu Ile Asp
 1 5 10 15
 Trp Asn Lys Pro
 20

10

(2) INFORMATION FOR SEQ ID NO: 145:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

20 Met Gly Thr Gln Pro Pro Val Val Ala Gly Phe Thr Ile Pro Met Leu
 1 5 10 15
 Gly Tyr Thr Val Arg Val Leu Thr Phe His Leu Ser Cys Ser
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 146:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

35

Met Lys Ile Pro Val Leu Pro Ala Val Val Leu Leu Ser Leu Leu Val
 1 5 10 15

40

Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu Glu Ser
 20 25 30

Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn Thr Pro Phe
 35 40 45

45

Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala Asp Glu Phe Leu
 50 55 60

50

Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg Lys Leu Pro Phe Leu
 65 70 75 80

Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly Leu Arg Ser Ala Thr Pro
 85 90 95

55

Asp Ala Gln

60

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Met Val Trp Gly Leu Leu Leu Gly
 1 5

10

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

20 Met Leu Pro Leu Leu Ser Leu Leu Phe Leu Phe Phe Ser Thr Val Ser
 1 5 10 15

Ser Phe Cys Gly Met Pro Leu Arg Ala His Thr Arg Ala Xaa Ala His
 20 25 30

25

Thr Arg Thr Phe Ala Ser Arg
 35

30

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

40 Met Ile Cys Glu Thr Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg
 1 5 10 15

Leu Pro Pro Pro Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr
 20 25 30

45

Ile Glu Arg Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp
 35 40 45

Leu Pro Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile
 50 55 60

50

Ile Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 65 70 75 80

55

Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro Ser
 85 90 95

Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His Gln Ala
 100 105 110

60

Val Asp Ser Pro Thr Ser Val Ala Ser Val Asp Gly Pro Val Leu Met

287

115 120 125

Gly Ser Thr
130

5

(2) INFORMATION FOR SEQ ID NO: 150:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

15

Met Gly Ala Pro Ser Leu Thr Met Leu Leu Leu Lys Val Gln Pro
1 5 10 15

20

Arg Arg Thr Gln Ala Phe Asp Ala His Trp Val Gly Leu Pro Leu Leu
20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 151:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

35

Met Cys Leu Ile Phe Leu Leu Leu Leu Leu Ser Phe Ser
1 5 10

40

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

His Pro His Gln Asp Ser Gln Pro
1 5

50

(2) INFORMATION FOR SEQ ID NO: 153:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

60

288

Met Asn Thr Ser Tyr Ile Leu Arg Leu Thr Val Val Val Ser Val Val
 1 5 10 15

Ile Tyr Leu Ala Ile His Pro Leu Leu Ser Phe Ser Leu Glu Ser Pro
 5 20 25 30

Leu Leu Val Pro Trp Arg Asp Cys Cys Gln Asn Ile Trp Lys Ser Gly
 35 40 45

10 Ser Val Trp Tyr Lys Arg Trp Thr Leu Pro His Met Glu Val Cys Cys
 50 55 60

Gln Asp Leu His
 65

15

(2) INFORMATION FOR SEQ ID NO: 154:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

25 Met Leu Lys Ile Phe Lys Glu Trp Glu Asn Leu Asn Leu Ile Leu Thr
 1 5 10 15

Ser Ile Arg Ile Leu Glu Arg Gln Asn Met
 30 20 25

(2) INFORMATION FOR SEQ ID NO: 155:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Met Asp Cys Glu Val Asn Asn Gly Ser Ser Leu Arg Asp Glu Cys Ile
 1 5 10 15

45 Thr Asn Leu Leu Val Phe Gly Phe Leu Gln Ser Cys Ser Asp Asn Ser
 20 25 30

Phe Arg Arg Glu Leu Asp Ala Leu Gly His Glu Leu Pro Val Leu Ala
 35 40 45

50 Pro Gln Trp Glu Gly Tyr Asp Glu Leu Gln Thr Asp Gly Asn Arg Ser
 50 55 60

Ser His Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser Gln Glu
 55 65 70 75 80

Asp Ile Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser
 85 90 95

60 Met Asp Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala Leu Gln

289

100 105 110

Leu Arg Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp Leu Ala
115 120 125

5 Thr Ala Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met Glu Lys
130 135 140

Glu Lys Thr Met Leu Val Leu Ala Leu Leu Leu Ala Lys Lys Val Ala
10 145 150 155 160

Ser His Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn
165 170 175

15 Phe Ile Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala Arg Asn
180 185 190

Gly Met Asp
195

20

(2) INFORMATION FOR SEQ ID NO: 156:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

30 Met Ser Leu Ser Leu Val Ser Val Ser Val Gly Pro Ser Thr Leu Ala
1 5 10 15

35 Cys Ser Phe Leu Arg Pro Lys Ala Arg Pro Ser Lys Arg Ser Pro Arg
20 25 30

Asn Tyr Thr Asp Ser Thr Ser Pro Gly Gly Pro Arg Ala Pro Arg Gly
35 40 45

40 Gly Ala Trp Arg Leu Ser Ser Gln Gln Asn Ser Ser Pro Lys Gly Val
50 55 60

Ala Val Ala Lys Ala Ser Tyr Arg Pro Val Leu Cys Phe Leu Pro Gly
65 70 75 80

45 Pro Trp Ser Ser Xaa Pro Xaa Ala Phe Leu Ile
85 90

50

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

Met Gly Thr Leu Ser Ala Glu Cys Ser Gly Pro Ala Thr Leu Gly Leu
1 5 10 15

60

290

Cys Leu Val Val Pro Trp Asn Ser Ser Gly Leu Ser Gln Pro Pro
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

15 Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
 1 5 10 15

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
 20 25 30

20

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
 35 40 45

25 Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
 50 55 60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
 65 70 75 80

30 Gly Asp Leu Pro Asn Gly Arg Val Cys Pro Xaa
 85 90

35 (2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 1 5 10 15

45

Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 20 25 30

50 Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
 35 40 45

Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
 50 55 60

55 Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
 65 70 75 80

Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 85

60

(2) INFORMATION FOR SEQ ID NO: 160:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
 1 5 10 15
 Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
 20 25 30
 Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Glu Gln Glu Ser Gln
 35 40 45
 Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
 50 55 60
 Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Glu Arg Lys Ile Asn
 65 70 75 80
 Lys Met Thr Asp Lys Leu Lys Thr His Val Lys Ala Arg Thr Ala Gln
 85 90 95
 Leu Ala Lys Ile Lys Trp Val Ile Ser Val Ala Phe Tyr Val Leu Gln
 100 105 110
 Ala Ala Leu Met Ile Ser Leu Ile Trp Lys Tyr Tyr Ser Val Pro Val
 115 120 125
 Ala Val Val Pro Ser Lys Trp Ile Thr Pro Leu Asp Arg Leu Val Ala
 130 135 140
 Phe Pro Thr Arg Val Ala Gly Gly Val Gly Ile Thr Cys Trp Ile Leu
 145 150 155 160
 Val Cys Asn Lys Val Val Ala Ile Val Leu His Pro Phe Ser
 165 170

45

(2) INFORMATION FOR SEQ ID NO: 161:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Met Gly Lys Leu Ile Asn Ile Val Ile Arg Lys Pro Leu Leu Leu Leu
 1 5 10 15
 Leu Val Gln Cys Glu Asn Cys Cys Arg Lys Asn Met Leu Tyr Asn Ile
 20 25 30
 Phe Leu Asn Ile His Asn Ile His Lys Phe Ser Asn His

35

40

45

5 (2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Met Val Ala Ser Thr Leu Val Thr Asn Leu Phe Gly Val Ala Phe Ala
 1 5 10 15
 Thr Thr Ala Ala Thr Arg Ala
 20

20

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Met Leu Met Ala Pro Val Val Cys Leu Ser Phe Ser Pro Cys Pro Ala
 30 1 5 10 15
 Asp Thr Ser Leu Thr Gly Asp Gly Leu Lys Ala Gly Leu Glu Arg Gly
 20 25 30
 Xaa Ala Leu Val Thr Leu Phe Asp Ser Val Thr His Phe Leu Ala His
 35 35 40 45
 Thr Leu Phe Glu Leu Leu Asp Phe Gln Leu Ala Phe Leu Arg Ser Gly
 50 55 60
 Lys Gln Thr Ala Pro His
 65 70

45

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

50 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln
 55 1 5 10 15
 Val Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu
 20 25 30
 Ser Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn
 60

293

	35	40	45
5	Leu Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro 50 55 60		
	Asp Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe 65 70 75 80		
10	Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly 85 90 95		
	Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Arg Asn 100 105 110		
15	Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly 115 120 125		
	Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu 130 135 140		
20	Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser 145 150 155 160		
	Tyr Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr 165 170 175		
25	Ala Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr 180 185 190		
30	Val Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu 195 200 205		
	Trp Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr 210 215 220		
35	Tyr Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp 225 230 235 240		
	Val Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu 245 250 255		
40	Glu Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met 260 265 270		
45	Lys Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala 275 280 285		
	Leu Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile 290 295 300		
50	Val Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys 305 310 315 320		
55	Arg Phe Tyr		

(2) INFORMATION FOR SEQ ID NO: 165:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

	Met	Pro	Ser	Glu	Tyr	Thr	Tyr	Val	Lys	Leu	Arg	Ser	Asp	Cys	Ser	Arg	
	1				5					10					15		
10	Pro	Ser	Leu	Gln	Trp	Tyr	Thr	Arg	Ala	Gln	Ser	Lys	Met	Arg	Arg	Pro	
				20					25					30			
	Ser	Leu	Leu	Leu	Lys	Asp	Ile	Leu	Lys	Cys	Thr	Leu	Leu	Val	Phe	Gly	
			35					40					45				
15	Val	Trp	Ile	Leu	Tyr	Ile	Leu	Lys	Leu	Asn	Tyr	Thr	Thr	Glu	Glu	Cys	
		50					55					60					
	Asp	Met	Lys	Lys	Met	His	Tyr	Val	Asp	Pro	Asp	His	Val	Lys	Arg	Ala	
20		65				70				75						80	
	Gln	Lys	Tyr	Ala	Gln	Gln	Val	Leu	Gln	Lys	Glu	Cys	Arg	Pro	Lys	Phe	
					85				90						95		
25	Ala	Lys	Thr	Ser	Met	Ala	Leu	Leu	Phe	Glu	His	Arg	Tyr	Ser	Val	Asp	
				100					105					110			
	Leu	Leu	Pro	Phe	Val	Gln	Lys	Xaa	Pro	Lys	Asp	Ser	Glu	Ala	Glu	Ser	
			115					120					125				
30	Lys	Tyr	Asp	Pro	Pro	Phe	Gly	Phe	Arg	Lys	Phe	Ser	Ser	Lys	Val	Gln	
		130					135					140					
	Thr	Leu	Leu	Glu	Leu	Leu	Pro	Glu	His	Asp	Leu	Pro	Glu	His	Leu	Lys	
35		145				150				155					160		
	Ala	Lys	Thr	Cys	Arg	Arg	Cys	Val	Val	Ile	Gly	Ser	Gly	Gly	Ile	Leu	
				165						170					175		
40	His	Gly	Leu	Glu	Leu	Gly	His	Thr	Leu	Asn	Gln	Phe	Asp	Val	Val	Ile	
			180						185					190			
	Arg	Leu	Asn	Ser	Ala	Pro	Val	Glu	Gly	Tyr	Ser	Glu	His	Val	Gly	Asn	
		195					200					205					
45	Lys	Thr	Thr	Ile	Arg	Met	Thr	Tyr	Pro	Glu	Gly	Ala	Pro	Leu	Ser	Asp	
		210				215						220					
	Leu	Glu	Tyr	Tyr	Ser	Asn	Asp	Leu	Phe	Val	Ala	Val	Leu	Phe	Lys	Ser	
50		225				230					235				240		
	Val	Asp	Phe	Asn	Trp	Leu	Gln	Ala	Met	Val	Lys	Lys	Glu	Thr	Leu	Pro	
				245					250					255			
55	Phe	Trp	Val	Arg	Leu	Phe	Phe	Trp	Lys	Gln	Val	Ala	Glu	Lys	Ile	Pro	
			260					265						270			
	Leu	Gln	Pro	Lys	His	Phe	Arg	Ile	Leu	Asn	Pro	Val	Ile	Ile	Lys	Glu	
60			275				280						285				

295

Thr Ala Phe Xaa His Pro Ser Val Leu Arg Ala Ser Val Lys Val Leu
 290 295 300

5 Gly Ala Glu Ile Arg Thr Ser Pro Gln Ser Val Ser Leu Pro Leu Ser
 305 310 315 320

Xaa

10

(2) INFORMATION FOR SEQ ID NO: 166:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

20 Met Thr Leu Asp Val Gln Thr Val Val Val Phe Ala Val Ile Val Val
 1 5 10 15

Leu Leu Leu Val Asn Val Ile Leu Met Phe Phe Leu Gly Thr Arg
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 167:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

35 Met Leu Pro Leu Leu Phe Cys Ala Phe Cys Leu His Lys Leu Gly Pro
 1 5 10 15

40 Leu Leu Phe Leu Tyr Asp Val Leu Met Xaa His Glu Ala Val Met Arg
 20 25 30

Thr His Gln Ile Gln Leu Pro Asp Pro Glu Phe Pro Ser Gln Gln Asn
 35 40 45

45 Gln Val Leu Asn Lys Thr Leu Phe Asn Lys Leu Lys Lys Lys Lys Lys
 50 55 60

Lys Lys Lys Xaa Xaa Xaa Lys Lys
 65 70

50

(2) INFORMATION FOR SEQ ID NO: 168:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

60

296

Met Ala Ser Arg Gly Arg Arg Pro Glu His Gly Gly Pro Pro Glu Leu
 1 5 10 15
 Phe Tyr Asp Glu Thr Glu Ala Arg Lys Tyr Val Arg Asn Ser Arg Met
 5 20 25 30
 Ile Asp Ile Gln Thr Arg Met Ala Gly Arg Ala Leu Glu Leu Leu Tyr
 35 40 45
 Leu Pro Glu Asn Lys Pro Cys Tyr Leu Leu Asp Ile Gly Cys Gly Thr
 10 50 55 60
 Gly Leu Ser Gly Ser Tyr Leu Ser Asp Glu Gly His Tyr Trp Val Gly
 65 70 75 80
 Leu Asp Ile Ser Pro Ala Met Leu Asp Glu Ala Val Asp Arg Glu Ile
 85 90 95
 Glu Gly Asp Leu Leu Leu Gly Asp Met Gly Gln Gly Ile Pro Phe Lys
 100 105 110
 Pro Gly Thr Phe Asp Gly Cys Ile Ser Ile Ser Ala Val Gln Trp Leu
 115 120 125
 Cys Asn Ala Asn Lys Lys Ser Glu Asn Pro Ala Lys Arg Leu Tyr Cys
 130 135 140
 Phe Phe Ala Ser Leu Phe Ser Val Leu Val Arg Gly Ser Arg Ala Val
 145 150 155 160
 Leu Gln Leu Tyr Pro Glu Asn Ser Glu Gln Leu Glu Leu Ile Thr Thr
 165 170 175
 Gln Ala Thr Lys Ala Gly Phe Ser Gly Gly Met Val Val Asp Tyr Pro
 180 185 190
 Asn Ser Ala Lys Ala Lys Lys Phe Tyr Leu Cys Leu Phe Ser Gly Pro
 195 200 205
 Ser Thr Phe Ile Pro Glu Gly Leu Ser Glu Asn Gln Asp Glu Val Glu
 210 215 220
 Pro Arg Glu Ser Val Phe Thr Asn Glu Arg Phe Pro Leu Arg Met Ser
 225 230 235 240
 Arg Arg Gly Met Val Arg Lys Ser Arg Ala Trp Val Leu Glu Lys Lys
 245 250 255
 Glu Arg His Arg Arg Gln Gly Arg Glu Val Arg Pro Asp Thr Gln Tyr
 260 265 270
 Thr Gly Arg Lys Arg Lys Pro Arg Phe Xaa
 275 280

55

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 amino acids

297

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5 Met Leu Gly Lys Thr Lys Phe Gln Ser Tyr Lys Ser Phe Ser Arg Lys
 1 5 10 15

Leu Met Val Cys Pro Ser Thr
 20

10

(2) INFORMATION FOR SEQ ID NO: 170:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

20

Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His Gly
 1 5 10 15

25

Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly Arg
 20 25 30

Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala His
 35 40 45

30

Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val Ala
 50 55 60

Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu Gly
 65 70 75 80

35

Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp Val
 85 90 95

40

Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg His
 100 105 110

Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp Arg
 115 120 125

45

Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly His
 130 135 140

Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr Tyr
 145 150 155 160

50

Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp Gln
 165 170 175

55

Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu His
 180 185 190

Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr Leu
 195 200 205

60

Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu Tyr

298

210 215 220

Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala Trp
 225 230 235 240

5 Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn Lys
 245 250 255

10 Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro Pro
 260 265 270

Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu Ser
 275 280 285

15 Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Xaa Ile Leu Gly Asn
 290 295 300

Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp Leu
 305 310 315 320

20 Thr Arg His His Asp Glu Leu Xaa
 325

25

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

35 Met Cys Trp Leu Arg Ala Trp Xaa Gln Ile Xaa Leu Pro Val Phe Xaa
 1 5 10 15

Ser Xaa Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly Phe
 20 25 30

40 Ile His Ser Pro Arg Asn Asn Gln Lys Pro Arg Asp Gly Asn Xaa Glu
 35 40 45

Glu Cys Ala Val Lys Lys Ser Cys Gln Leu Cys Thr Glu Asp Lys Lys
 50 55 60

45 Tyr Met Met Asn Arg
 65

50

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

60 Met Trp Leu Phe Ile Leu Leu Ser Leu Ala Leu Ile Ser Asp Ala Met
 1 5 10 15

Val Met Asp Glu Lys Val Lys Arg Ser Phe Val Leu Asp Thr Ala Ser
 20 25 30

5 Ala Ile Cys Asn Tyr Asn Ala His Tyr Lys Asn His Pro Lys Tyr Trp
 35 40 45

Cys Arg Gly Tyr Phe Arg Asp Tyr Cys Asn Ile Ile Ala Phe Ser Pro
 50 55 60

10 Asn Ser Thr Asn His Val Ala Leu Lys Asp Thr Gly Asn Gln Leu Ile
 65 70 75 80

15 Val Thr Met Ser Cys Leu Asn Lys Glu Asp Thr Gly Trp Tyr Trp Cys
 85 90 95

Gly Ile Gln Arg Asp Phe Ala Arg Asp Asp Met Asp Phe Thr Glu Leu
 100 105 110

20 Ile Val Thr Asp Asp Lys Gly Thr Trp Pro Met Thr Leu Val Trp Glu
 115 120 125

Arg Leu Ser Gly Thr Lys Pro Glu Ala Ala Arg Leu Pro Lys Leu Ser
 130 135 140

25 Ala Arg Leu Thr Ala Pro Gly Arg Pro Phe Ser Ser Phe Ala Tyr Xaa
 145 150 155 160

30

35 (2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Met Ala Xaa His Phe Leu Leu Val Ala Leu Gln Ser Val Pro His Cys
 1 5 10 15

45 Pro His Leu Leu Glu Glu Glu His Lys Leu Cys Lys Val Ser His Phe
 20 25 30

Ser Gly Val Thr Leu Val Thr Ser Arg Gln Asp Ser Ser Ser Tyr Val
 35 40 45

50 Pro Val Gln Thr Leu Phe Ile His Leu Gly Pro Trp Ala Trp Asp Leu
 50 55 60

55 Xaa Pro Cys Thr Ala Glu Asp Pro Glu Ala Glu Arg Ser Leu Arg Leu
 65 70 75 80

Cys His Ser His Leu Ala Arg Xaa Asn Val Ser Pro Ser Gln Ala Ala
 85 90 95

60 Glu Gly Xaa Xaa Xaa Arg Gly Cys Gln His Arg Gly Ser Arg Glu Leu

300

100 105 110

Thr Phe Leu Ser Ala Glu Asn Glu Ala Gly Ile
115 120

5

(2) INFORMATION FOR SEQ ID NO: 174:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

15 Met Lys Val Gly Ala Arg Ile Arg Val Lys Met Ser Val Asn Lys Ala
1 5 10 15

20 His Pro Val Val Ser Thr His Trp Arg Trp Pro Ala Glu Trp Pro Gln
20 25 30

Met Phe Leu His Leu Ala Gln Glu Pro Arg Thr Glu Val Lys Ser Arg
35 40 45

25 Pro Leu Gly Leu Ala Gly Phe Ile Arg Gln Asp Ser Lys Thr Arg Lys
50 55 60

Pro Leu Glu Gln Glu Thr Ile Met Ser Ala Ala Asp Thr Ala Leu Trp
65 70 75 80

30 Pro Tyr Gly His Gly Asn Arg Glu His Gln Glu Asn Glu Leu Gln Lys
85 90 95

35 Tyr Leu Gln Tyr Lys Asp Met His Leu Leu Asp Ser Gly Gln Ser Leu
100 105 110

Gly His Thr His Thr Leu Gln Gly Ser His Asn Leu Thr Ala Leu Asn
115 120 125

40 Ile

45 (2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
1 5 10 15

55 Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
20 25 30

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
35 40 45

60

301

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
 50 55 60

5 Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
 65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
 85 90 95

10 Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
 100 105 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
 115 120 125

15 Asn Asp Trp Trp Val Cys Lys His Ile Lys Lys Pro Ile Arg Ser Thr
 130 135 140

20 Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly
 145 150 155 160

Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val
 165 170 175

25 Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
 180 185 190

Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val
 195 200 205

30 Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp Ser
 210 215 220

35 Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu
 225 230 235 240

Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn
 245 250 255

40 Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr
 260 265 270

Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro
 275 280 285

Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn
 290 295 300

50 Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly
 305 310 315 320

Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser
 325 330 335

55 Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly
 340 345 350

Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp
 355 360 365

Leu Lys Ile Lys
370

5

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

15 Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu
 1 5 10 15

Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala
 20 25 30

Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro
 35 40 45

Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile
 25 50 55 60

Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala
 65 70 75 80

30 Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu
 85 90 95

Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln
 100 105 110

35 Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr
 115 120 125

Gly Pro Gln Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly
 40 130 135 140

Val Trp Tyr Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn
 145 150 155 160

45 Leu Glu Gly Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser
 165 170 175

Gly Lys Gln Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp
 180 185 190

50 Lys Val Asn Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro
 195 200 205

Gln Thr Leu Ala Ser Glu Lys Lys
 55 210 215

60

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Met Lys Pro Val Ser Arg Arg Thr Leu Asp Trp Ile Tyr Ser Val Leu
 1 5 10 15

10 Leu Leu Ala Ile Val Leu Ile Ser Trp Gly Cys Ile Ile Tyr Ala Ser
 20 25 30

Met Val Ser Ala Arg Arg Gln Leu Arg Lys Lys Tyr Pro Asp Lys Ile
 35 40 45

15 Phe Gly Thr Asn Glu Asn Leu
 50 55

20

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

30 Met Ala Ala Asn Thr Phe Val Leu Ile Met Gly Ile Pro Thr Ser Ala
 1 5 10 15

Asn Ala Xaa Arg Asp Leu Phe
 20

35

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

45 Met Ser Ile Cys His Arg Gly Thr Gly Ile Ala Leu Ser Ala Gly Val
 1 5 10 15

Ser Leu Phe Gly Met Ser Ala Leu Leu Leu Pro Gly Asn Phe Glu Ser
 20 25 30

50

Tyr Leu Glu Leu Val Lys Ser Leu Cys Leu Gly Pro Ala Leu Ile His
 35 40 45

55 Thr Ala Lys Phe Ala Leu Val Phe Pro Leu Met Tyr His Thr Trp Asn
 50 55 60

Gly Ile Arg His Leu Met Trp Asp Leu Gly Lys Gly Leu Lys Ile Pro
 65 70 75 80

60 Gln Leu Tyr Gln Ser Gly Val Val Val Leu Val Leu Thr Val Leu Ser

304

85

90

95

Ser Met Gly Leu Ala Ala Met
100

5

(2) INFORMATION FOR SEQ ID NO: 180:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

15

Met Thr Lys Ala Ser Ser Leu Trp Pro Leu Lys Thr Thr Cys Gln Ile
1 5 10 15

20

Ser Gly Thr Val Phe Phe Phe Leu Phe Leu Phe Ser Cys Phe Leu Met
20 25 30

Gln Ala Gln Cys Asp Lys Phe Val Gly Trp Asp Phe Phe Phe Phe Leu
35 40 45

25

30

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

35

Met Arg Arg Ala Leu Ile Pro Pro Cys Arg Gly Gly Pro Ser Ala Ser
1 5 10 15

40

Asp Xaa Cys Cys Ser Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly
20 25 30

45

Arg Cys Pro Val Gln Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu
35 40 45

Arg Arg Trp Gly Pro Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly
50 55 60

50

Phe Gln Leu Leu Arg Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro
65 70 75 80

Arg Lys Gly Pro Phe Pro Pro Pro Asp Pro Pro Trp Pro Val Thr Leu
85 90 95

55

60

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

5 Met Leu Glu Thr Thr Lys His Val Gln Ile Ala Cys Met Leu Leu Leu
 10 1 5 10 15
 Thr Cys Gln Ile Phe Leu Pro Ser Ser Leu Ser Pro Ser Phe Ile His
 20 25 30
 15 Ser Leu Thr Asp Ser Phe Ile Pro Leu Lys Lys Leu Tyr Val Cys Phe
 35 40 45
 Val Gln Ser Thr Leu Leu Lys Ala Ala Gly Tyr Lys Ser Ile Ser Glu
 50 55 60
 20 Ala Leu Gly Phe Asp Xaa Leu Leu Cys Ser Ser Ala Arg Phe Val Trp
 65 70 75 80
 25 Ile Cys His Thr Tyr Ser Arg Pro Leu Val Thr Cys Ala Leu His
 85 90 95

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

30 Met Ser Val Ile Gly Gly Leu Leu Leu Val Val Ala Leu Gly Pro Gly
 1 5 10 15
 40 Gly Val Ser Met Asp Glu Lys Lys Lys Glu Trp
 20 25

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

50 Met Ser Gly Gly Leu Ser Phe Leu Leu Leu Val
 1 5 10
 55

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

60

306

(A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

5 Met Phe Ala Asp Phe Ile Val Val Thr Ala Thr Val Gln Arg Cys Pro
 1 5 10 15
 10 Gly Ser Pro Pro Leu Ser Glu Ile Leu Trp Lys Asp Glu Pro Phe Ala
 20 25 30
 Ile Ser Ser His Ala Gly Leu Pro Trp Leu Ser Ser Trp Pro Ala Pro
 35 40 45
 15 Pro Trp Thr Trp Ser Trp Ile Ser Arg Arg Arg Glu His Gly Arg Gly
 50 55 60
 Ser
 65
 20

(2) INFORMATION FOR SEQ ID NO: 186:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

30 Met Val Glu Ser Val Met Pro Val Val Val Cys Thr Leu Ser Pro Gly
 1 5 10 15
 35 Ile Asp Ser Ser Pro Ser
 20

(2) INFORMATION FOR SEQ ID NO: 187:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
 1 5 10 15
 50 Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
 20 25 30
 Val Val Tyr Tyr Tyr Thr Val Thr Pro Ser Tyr Asp Asp Phe Ser Ala
 35 40 45
 55 Asp Phe Thr Ile Asp Tyr Ser Ile Phe Glu Ser Glu Asp Arg Leu Asn
 50 55 60
 Arg Leu Asp Lys Asp Ile Thr Glu Ala Ile Glu Thr Thr Ile Ser Leu
 65 70 75 80

307

Glu Thr Ala Arg Ala Asp His Pro Lys Pro Val Thr Val Lys Pro Val
 85 90 95
 5 Thr Thr Glu Pro Gln Ser Pro Asp Leu Asn Asp Ala Val Ser Ser Leu
 100 105 110
 Arg Ser Pro Ile Pro Leu Leu Leu Ser Cys Ala Phe Val Gln Val Gly
 115 120 125
 10 Met Tyr Phe Met
 130

15

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 20 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

25 Met Pro Cys Gln Pro Gly Gln Val Pro Ser Cys Gln Cys Thr Phe Gly
 1 5 10 15
 Leu Leu Leu Met Leu Pro Ser Leu Pro Ser Pro Ala Ser Gln Pro Arg
 20 25 30
 30 Pro Phe Cys Ser Ser Met Glu Tyr Phe His Gly Cys Ala Ser Pro Ser
 35 40 45
 Gln Ala Ile Ile Gly Gly Phe Pro Phe Ala Ser Val Ala Leu Ala Asp
 50 55 60
 35 Ile Leu Cys Leu Gln
 65

40

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 45 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

50 Met Ser Leu Leu Ser Pro Ala Ile Pro Ala Leu Thr Leu Ile Phe Ile
 1 5 10 15
 Leu Met Phe Phe Ser Phe Pro Phe Arg Ala His Thr Val Val Thr Ile
 20 25 30
 55 Val Ala Ser Gly Phe Leu Gly Leu Ser Pro Leu Cys Gly
 35 40 45

60

(2) INFORMATION FOR SEQ ID NO: 190:

308

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
 1 5 10 15
 Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
 20 25 30
 Tyr Gly Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu
 35 40 45
 Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Arg
 50 55 60
 Ser
 65

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met Leu Lys
 1 5 10 15
 Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser Phe Ile Ser Phe
 20 25 30
 Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met Met Ser Ser Phe
 35 40 45
 Met Xaa
 50

45

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Leu Leu Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala Tyr
 1 5 10 15
 Arg Leu Trp Val Arg Trp Gly Arg Arg Gly Leu Gly Ala Gly
 20 25 30

60

309

Ala Gly Glu Glu Ser Pro Ala Thr Ser Leu Pro Arg Met Lys Lys Arg
 35 40 45

5 Asp Phe Ser Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ser Arg Asn Pro
 50 55 60

Arg Ile Leu Leu Ala Val Asn Gly Lys Val Phe Asp Val Thr Lys Gly
 65 70 75 80

10 Ser Lys Phe Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly Arg
 85 90 95

Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu
 100 105 110

15 Arg Asp Glu Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu
 115 120 125

Ser Val Arg Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val
 130 135 140

20 Gly Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp Glu
 145 150 155 160

25 Glu Asp Thr Lys Asp His Asn Lys Gln Asp
 165 170

30 (2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Met Thr Tyr Phe Ser Gly Leu Leu Val Ile Leu Ala Phe Ala Ala Trp
 1 5 10 15

40 Val Ala Leu Ala Glu Gly Leu Gly Val Ala Val Tyr Ala Ala Ala Val
 20 25 30

Leu Leu Gly Ala Gly Cys Ala Thr Ile Leu Val Thr Ser Leu Ala Met
 35 40 45

45 Thr Ala Asp Leu Ile Gly Pro His Thr Asn Ser Gly Leu Ser Cys Thr
 50 55 60

50 Ala Pro
 65

55 (2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

5 Met Ala Ala Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu Arg
 1 5 10 15
 Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu
 20 25 30
 10 Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu
 35 40 45
 Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp
 50 55 60
 15 Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys
 65 70 75 80
 Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly
 85 90

(2) INFORMATION FOR SEQ ID NO: 195:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

30 Met Arg Gly Ser His Leu Arg Leu Leu Pro Tyr Leu Val Ala Ala Asn
 1 5 10 15
 35 Pro Val Asn Tyr Gly Arg Pro Tyr Arg Leu Ser Cys Val Glu Ala Phe
 20 25 30
 Ala Ala Thr Phe Cys Ile Val Gly Phe Pro Asp Leu Ala Val Ile Leu
 35 40 45
 40 Leu Arg Lys Phe Lys Trp Gly Lys Gly Phe Leu Asp Leu Asn Arg Gln
 50 55 60
 Leu Leu Asp Lys Tyr Ala Ala Cys Gly Ser Pro Glu Glu Val Leu Gln
 65 70 75 80
 45 Ala Glu Gln Glu Phe Leu Ala Asn Ala Lys Glu Ser Pro Gln Glu Glu
 85 90 95
 50 Glu Ile Asp Pro Phe Asp Val Asp Ser Gly Arg Glu Phe Gly Asn Pro
 100 105 110
 Asn Arg Pro Val Ala Ser Thr Arg Leu Pro Ser Asp Thr Asp Asp Ser
 115 120 125
 55 Asp Ala Ser Glu Asp Pro Gly Pro Xaa Ala Glu Arg Gly Gly Ala Ser
 130 135 140
 Ser Ser Cys Cys Glu Glu Glu Gln Thr Gln Gly Arg Gly Ala Glu Ala
 145 150 155 160

Arg Ala Pro Ala Glu Val Trp Lys Gly Ile Lys Lys Arg Gln Arg Asp
 165 170 175

5

(2) INFORMATION FOR SEQ ID NO: 196:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Met Ser Asn Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr Gly Ile
 1 5 10 15

20

Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg Ala His Leu
 20 25 30

Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly Asn Thr Val Ile
 35 40 45

25

Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe Gly Ser Asn Asp Asp
 50 55 60

30

Phe Ser Trp Gln Gln Trp
 65 70

(2) INFORMATION FOR SEQ ID NO: 197:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Met Thr Leu Leu Ile Ile Phe Leu Pro Phe Xaa Phe Thr Thr Xaa Thr
 1 5 10 15

45

Asn Ser Gly Gly Ser Phe Pro Val Arg
 20 25

(2) INFORMATION FOR SEQ ID NO: 198:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Met Lys Gly Glu Leu Leu Pro Phe Leu Phe Leu Thr Val Trp Leu Trp
 1 5 10 15

60

Leu Tyr Lys Leu Xaa Phe Gly Glu Ser Pro Arg Tyr Pro Asn Val Ile
 20 25 30
 5 Gly Lys Thr Tyr Phe Phe Phe Trp Thr Asp Gln Ile Ser Arg Glu Ser
 35 40 45
 Arg Phe Leu Glu Arg Leu Ala Phe Ile Val Ser Glu Asn Cys Leu Ile
 50 55 60
 10 Phe Leu Ile His Ala Ile Thr Gly Gln
 65 70

15 (2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu
 1 5 10 15
 25 Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
 20 25 30
 His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val
 35 40 45
 30 Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp
 50 55 60
 35 Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr
 65 70 75 80
 Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala
 85 90 95
 40 Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly
 100 105 110
 45 Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys
 115 120 125
 Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu
 130 135 140
 50 Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn
 145 150 155 160
 Val Asp Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys
 165 170 175
 55 Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg
 180 185 190
 60 Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala
 195 200 205

Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His
 210 215 220
 5 Asp His Trp Lys Ala Leu Val Thr Lys Lys Thr Asn Gly Lys Gly Ile
 225 230 235 240
 Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro
 245 250 255
 10 Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser
 260 265 270
 Ala Cys Thr Val Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys
 15 275 280 285
 Asn
 20
 (2) INFORMATION FOR SEQ ID NO: 200:
 (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 625 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:
 30 Met Glu Ile Pro Gly Ser Leu Cys Lys Lys Val Lys Leu Ser Asn Asn
 1 5 10 15
 Ala Gln Asn Trp Gly Met Gln Arg Ala Thr Asn Val Thr Tyr Gln Ala
 20 25 30
 35 His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly Thr Arg Gly
 35 40 45
 Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser Gly Ala Gly
 40 50 55 60
 Lys Thr Thr Val Ser Met Ala Leu Glu Glu Tyr Leu Val Cys His Gly
 65 70 75 80
 45 Ile Pro Cys Tyr Thr Leu Asp Gly Asp Asn Ile Arg Gln Gly Leu Asn
 85 90 95
 Lys Asn Leu Gly Phe Ser Pro Glu Asp Arg Glu Glu Asn Val Arg Arg
 100 105 110
 50 Ile Ala Glu Val Ala Lys Leu Phe Ala Asp Ala Gly Leu Val Cys Ile
 115 120 125
 Thr Ser Phe Ile Ser Pro Tyr Thr Gln Asp Arg Asn Asn Ala Arg Gln
 130 135 140
 55 Ile His Glu Gly Ala Ser Leu Pro Phe Phe Glu Val Phe Val Asp Ala
 145 150 155 160
 60 Pro Leu His Val Cys Glu Gln Arg Asp Val Lys Gly Leu Tyr Lys Lys

315

485 490 495

Tyr Ala Gly Pro Thr Glu Val Gln Trp His Cys Arg Ala Arg Met Val
500 505 510

5 Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Pro
515 520 525

10 His Pro Glu Thr Gly Lys Asp Leu Tyr Glu Pro Ser His Gly Ala Lys
530 535 540

Val Leu Thr Met Ala Pro Gly Leu Ile Thr Leu Glu Ile Val Pro Phe
545 550 555 560

15 Arg Val Ala Ala Tyr Asn Lys Lys Lys Lys Arg Met Asp Tyr Tyr Asp
565 570 575

Ser Glu His His Glu Asp Phe Glu Phe Ile Ser Gly Thr Arg Met Arg
580 585 590

20 Lys Leu Ala Arg Glu Gly Gln Lys Pro Pro Glu Gly Phe Met Ala Pro
595 600 605

Lys Ala Trp Thr Val Leu Thr Glu Tyr Tyr Lys Ser Leu Glu Lys Ala
610 615 620

25 Xaa
625

30

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 649 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

40 Met Ser Ala Ser Gln Asp Leu Glu Pro Lys Pro Leu Phe Pro Lys Pro
1 5 10 15

Ala Phe Gly Gln Lys Pro Pro Leu Ser Thr Glu Asn Ser His Glu Asp
20 25 30

45 Glu Ser Pro Met Lys Asn Val Ser Ser Ser Lys Gly Ser Pro Ala Pro
35 40 45

50 Leu Gly Val Arg Ser Lys Ser Gly Pro Leu Lys Pro Ala Arg Glu Asp
50 55 60

Ser Glu Asn Lys Asp His Ala Gly Glu Ile Ser Ser Leu Pro Phe Pro
65 70 75 80

55 Gly Val Val Leu Lys Pro Ala Ala Ser Arg Gly Gly Pro Gly Leu Ser
85 90 95

Lys Asn Gly Glu Glu Lys Lys Glu Asp Arg Lys Ile Asp Ala Ala Lys
100 105 110

60

316

Asn Thr Phe Gln Ser Lys Ile Asn Gln Glu Glu Leu Ala Ser Gly Thr
 115 120 125
 5 Pro Pro Ala Arg Phe Pro Lys Ala Pro Ser Lys Leu Thr Val Gly Gly
 130 135 140
 Pro Trp Gly Gln Ser Gln Glu Lys Glu Lys Gly Asp Lys Asn Ser Ala
 145 150 155 160
 10 Thr Pro Lys Gln Lys Pro Leu Pro Pro Leu Phe Thr Leu Gly Pro Pro
 165 170 175
 Pro Pro Lys Pro Asn Arg Pro Pro Asn Val Asp Leu Thr Lys Phe His
 180 185 190
 15 Lys Thr Ser Ser Gly Asn Ser Thr Ser Lys Gly Gln Thr Ser Tyr Ser
 195 200 205
 20 Thr Thr Ser Leu Pro Pro Pro Pro Pro Ser His Pro Ala Ser Gln Pro
 210 215 220
 Pro Leu Pro Ala Ser His Pro Ser Gln Pro Pro Val Pro Ser Leu Pro
 225 230 235 240
 25 Pro Arg Asn Ile Lys Pro Pro Phe Asp Leu Lys Ser Pro Val Asn Glu
 245 250 255
 Asp Asn Gln Asp Gly Val Thr His Ser Asp Gly Ala Gly Asn Leu Asp
 260 265 270
 30 Glu Glu Gln Asp Ser Glu Gly Glu Thr Tyr Glu Asp Ile Glu Ala Ser
 275 280 285
 35 Lys Glu Arg Glu Lys Lys Arg Glu Lys Glu Glu Lys Lys Arg Leu Glu
 290 295 300
 Leu Glu Lys Lys^{*} Glu Gln Lys Glu Lys Glu Lys Lys Glu Gln Glu Ile
 305 310 315 320
 40 Lys Lys Lys Phe Lys Leu Thr Gly Pro Ile Gln Val Ile His Leu Ala
 325 330 335
 Lys Ala Cys Cys Asp Val Lys Gly Gly Lys Asn Glu Leu Ser Phe Lys
 340 345 350
 45 Gln Gly Glu Gln Ile Glu Ile Ile Arg Ile Thr Asp Asn Pro Glu Gly
 355 360 365
 50 Lys Trp Leu Gly Arg Thr Ala Arg Gly Ser Tyr Gly Tyr Ile Lys Thr
 370 375 380
 Thr Ala Val Glu Ile Asp Tyr Asp Ser Leu Lys Leu Lys Lys Asp Ser
 385 390 395 400
 55 Leu Gly Ala Pro Ser Arg Pro Ile Glu Asp Asp Gln Glu Val Tyr Asp
 405 410 415
 Asp Val Ala Glu Gln Asp Asp Ile Ser Ser His Ser Gln Ser Gly Ser
 420 425 430
 60

317

Gly Gly Ile Phe Pro Pro Pro Pro Asp Asp Asp Ile Tyr Asp Gly Ile
 435 440 445
 5 Glu Glu Glu Asp Ala Asp Asp Gly Ser Thr Leu Gln Val Gln Glu Lys
 450 455 460
 Ser Asn Thr Trp Ser Trp Gly Ile Leu Lys Met Leu Lys Gly Lys Asp
 465 470 475 480
 10 Asp Arg Lys Lys Ser Ile Arg Glu Lys Pro Lys Val Ser Asp Ser Asp
 485 490 495
 Asn Asn Glu Gly Ser Ser Phe Pro Ala Pro Pro Lys Gln Leu Asp Met
 500 505 510
 15 Gly Asp Glu Val Tyr Asp Asp Val Asp Thr Ser Asp Phe Pro Val Ser
 515 520 525
 Ser Ala Glu Met Ser Gln Gly Thr Asn Val Gly Lys Ala Lys Thr Glu
 20 530 535 540
 Glu Lys Asp Leu Lys Lys Leu Lys Lys Gln Xaa Lys Xaa Xaa Lys Asp
 545 550 555 560
 25 Phe Arg Lys Lys Phe Lys Tyr Asp Gly Glu Ile Arg Val Leu Tyr Ser
 565 570 575
 Thr Lys Val Thr Thr Ser Ile Thr Ser Lys Lys Trp Gly Thr Arg Asp
 580 585 590
 30 Leu Gln Val Lys Pro Gly Glu Ser Leu Glu Val Ile Gln Thr Thr Asp
 595 600 605
 Asp Thr Lys Val Leu Cys Arg Asn Glu Glu Gly Lys Tyr Gly Tyr Val
 35 610 615 620
 Leu Arg Ser Tyr Leu Ala Asp Asn Asp Gly Glu Ile Tyr Asp Asp Ile
 625 630 635 640
 40 Ala Asp Gly Cys Ile Tyr Asp Asn Asp
 645

45 (2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Met Ala Trp Pro Ser Arg Ser Lys Met Phe Thr Leu Leu Pro Val Leu
 1 5 10 15
 55 Cys Tyr Leu Trp Ser Leu Trp Leu Pro Gln Phe Ser Trp Ile Gln Glu
 20 25 30
 60 Leu Lys Ala Val Leu Arg Asp Asp Gly Leu Ile Ser Ala Val Ala Trp
 35 40 45

Asn Ala Glu Phe Gln Thr Cys
50 55

5

(2) INFORMATION FOR SEQ ID NO: 203:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

15

Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu Ala Lys
1 5 10 15

Lys Asp Glu Pro Lys Ser Gly Glu Glu Ala Leu Ile Ile Pro Pro Asp
20 25 30

20

Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly
35 40 45

25

Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met
50 55 60

Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala
65 70 75 80

30

Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp
85 90 95

Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr
100 105 110

35

Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu Val Glu
115 120 125

40

Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro Ala Asn
130 135 140

Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp Leu Asn
145 150 155 160

45

Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val Met Pro
165 170 175

Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly Thr Tyr
180 185 190

50

Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr Asp Arg
195 200 205

55

Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu Cys His
210 215 220

Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly Ile
225 230 235 240

60

Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe Glu Asn

319

245 250 255
 Lys Phe Ala Val Glu Thr Leu Ile Cys Ser Xaa
 260 265
 5
 (2) INFORMATION FOR SEQ ID NO: 204:
 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:
 15 Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 1 5 10 15
 20 Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
 20 25 30
 Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp
 35 40 45
 25 His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Thr Phe Asp Gln Leu
 50 55 60
 Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
 65 70 75 80
 30 Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys Asp Trp
 85 90 95
 Ile Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln
 35 100 105 110
 Trp Lys Gly His Asp Leu Asn Glu Asp Gly Leu Val Ser Trp Glu Glu
 115 120 125
 40 Tyr Lys Asn Ala Thr Tyr Gly Tyr Val Leu Asp Asp Pro Asp Pro Asp
 130 135 140
 Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe
 145 150 155 160
 45 Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe
 165 170 175
 Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
 50 180 185 190
 Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
 195 200 205
 55 Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
 210 215 220
 Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
 225 230 235 240
 60

320

Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Glu Thr Lys Asp
 245 250 255

5 Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His
 260 265 270

Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu
 275 280 285

10 Glu Ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp
 290 295 300

Phe Gly Glu Ala Leu Val Arg His Asp Glu Phe
 305 310 315

15

(2) INFORMATION FOR SEQ ID NO: 205:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

25 Met Phe Asp Ala Val Leu Ile Leu Leu Ile Pro Leu Lys Asp Lys
 1 5 10 15

30 Leu Val Asp Pro Ile Leu Arg Arg His Gly Leu Leu Pro Ser Ser Leu
 20 25 30

Lys Arg Ile Ala Val Gly Met Phe Phe Val Met Cys Ser Ala Phe Ala
 35 40 45

35 Ala Gly Ile Leu Glu Ser Lys Arg Leu Asn Leu Val Lys Glu Lys Thr
 50 55 60

Ile Asn Gln Thr Ile Gly Asn Val Val Tyr His Ala Ala Asp Leu Ser
 65 70 75 80

40 Leu Trp Trp Gln Val Pro Gln Tyr Leu Leu Ile Gly Ile Ser Glu Ile
 85 90 95

Phe Ala Ser Ile Ala Gly Leu Glu Phe Ala Tyr Ser Ala Ala Pro Lys
 45 100 105 110

Ser Met Gln Ser Ala Ile Met Gly Leu Phe Phe Phe Phe Ser Gly Val
 115 120 125

50 Gly Ser Phe Val Gly Ser Gly Leu Leu Ala Leu Val Ser Ile Lys Ala
 130 135 140

Ile Gly Trp Met Ser Ser His Thr Asp Phe Gly Asn Ile Asn Gly Cys
 145 150 155 160

55 Tyr Leu Asn Tyr Tyr Phe Phe Leu Leu Ala Ile Gln Gly Ala Thr
 165 170 175

60 Leu Leu Leu Phe Leu Ile Ile Ser Val Lys Tyr Asp His His Arg Asp
 180 185 190

321

His Gln Arg Ser Arg Ala Asn Gly Val Pro Thr Ser Arg Arg Ala
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

15 Met Arg Ser Arg Ile Arg Glu Phe Asp Ser Ser Thr Leu Asn Glu Ser
 1 5 10 15
 Val Arg Asn Thr Ile Met Arg Asp Leu Lys Ala Val Gly Lys Lys Phe
 20 25 30
 Met His Val Leu Tyr Pro Arg Lys Ser Asn Thr Leu Leu Arg Asp Trp
 35 40 45
 Asp Leu Trp Gly Pro Leu Ile Leu Cys Val Thr Leu Ala Leu Met Leu
 25 50 55 60
 Gln Arg Asp Ser Ala Asp Ser Glu Lys Asp Gly Gly Pro Gln Phe Ala
 65 70 75 80
 30 Glu Val Phe Val Ile Val Trp Phe Gly Ala Val Thr Ile Thr Leu Asn
 85 90 95
 Ser Lys Leu Leu Gly Gly Asn Ile Ser Phe Phe Gln Ser Leu Cys Val
 100 105 110
 35 Leu Gly Tyr Cys Ile Leu Pro Leu Thr Val Ala Met Leu Ile Cys Arg
 115 120 125
 Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn Phe Met Val Arg Leu
 40 130 135 140
 Phe Val Val Ile Val Met Phe Ala Trp Ser Ile Val Ala Ser Thr Ala
 145 150 155 160
 45 Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg Ala Leu Ala Val Tyr
 165 170 175
 Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp Met Ile Leu Thr Phe
 180 185 190
 50 Thr Pro Gln Xaa
 195

55

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid

60

322

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

5	Met	Ala	Lys	Asp	Gln	Ala	Val	Glu	Asn	Ile	Leu	Val	Ser	Pro	Val	Val	1	5	10	15
	Val	Ala	Ser	Ser	Leu	Gly	Leu	Val	Ser	Leu	Gly	Gly	Lys	Ala	Thr	Thr	20	25	30	
10	Ala	Ser	Gln	Ala	Lys	Ala	Val	Leu	Ser	Ala	Glu	Gln	Leu	Arg	Asp	Glu	35	40	45	
	Glu	Val	His	Ala	Gly	Leu	Gly	Glu	Leu	Leu	Arg	Ser	Leu	Ser	Asn	Ser	50	55	60	
15	Thr	Ala	Arg	Asn	Val	Thr	Trp	Lys	Leu	Gly	Ser	Arg	Leu	Tyr	Gly	Pro	65	70	75	80
20	Ser	Ser	Val	Ser	Phe	Ala	Asp	Asp	Phe	Val	Arg	Ser	Ser	Lys	Gln	His	85	90	95	
	Tyr	Asn	Cys	Glu	His	Ser	Lys	Ile	Asn	Phe	Arg	Asp	Lys	Arg	Ser	Ala	100	105	110	
25	Leu	Gln	Ser	Ile	Asn	Glu	Trp	Ala	Ala	Gln	Thr	Thr	Asp	Gly	Lys	Leu	115	120	125	
	Pro	Glu	Val	Thr	Lys	Asp	Val	Glu	Arg	Thr	Asp	Gly	Ala	Leu	Leu	Val	130	135	140	
30	Asn	Ala	Met	Phe	Phe	Lys	Pro	His	Trp	Asp	Glu	Lys	Phe	His	His	Lys	145	150	155	160
35	Met	Val	Asp	Asn	Arg	Gly	Phe	Met	Val	Thr	Arg	Ser	Tyr	Thr	Val	Gly	165	170	175	
	Val	Met	Met	Met	His	Arg	Thr	Gly	Leu	Tyr	Asn	Tyr	Tyr	Asp	Asp	Glu	180	185	190	
40	Lys	Glu	Lys	Leu	Gln	Ile	Val	Glu	Met	Pro	Leu	Ala	His	Lys	Leu	Ser	195	200	205	
	Ser	Leu	Ile	Ile	Leu	Met	Pro	His	His	Val	Glu	Pro	Leu	Glu	Arg	Leu	210	215	220	
45	Glu	Lys	Leu	Leu	Thr	Lys	Glu	Gln	Leu	Lys	Ile	Trp	Met	Gly	Lys	Met	225	230	235	240
50	Gln	Lys	Lys	Ala	Val	Ala	Ile	Ser	Leu	Pro	Lys	Gly	Val	Val	Glu	Val	245	250	255	
	Thr	His	Asp	Leu	Gln	Lys	His	Leu	Ala	Gly	Leu	Gly	Leu	Thr	Glu	Ala	260	265	270	
55	Ile	Asp	Lys	Asn	Lys	Ala	Asp	Leu	Ser	Arg	Met	Ser	Gly	Lys	Lys	Asp	275	280	285	
60	Leu	Tyr	Leu	Ala	Ser	Val	Phe	His	Ala	Thr	Ala	Phe	Glu	Leu	Asp	Thr	290	295	300	

323

Asp Gly Asn Pro Leu Thr Arg Ile Thr Gly Gly Gly Val Arg Thr Gln
305 310 315 320

5 Val Phe Tyr Ala Asp His Pro Phe Ile Ser Xaa
325 330

10 (2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Met Cys Met Gln Leu Phe Gly Phe Leu Ala Phe Met Ile Phe Met Cys
1 5 10 15

20 Trp Val Gly Asp Val Tyr Pro Val Tyr Gln Pro Val Gly Pro Lys Gln
20 25 30

Tyr Pro Tyr Asn Asn Leu Tyr Leu Glu Arg Gly Gly Asp Pro Ser Lys
35 40 45

25 Glu Pro Glu Arg Val Val His Tyr Glu Ile
50 55

30 (2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

40 Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
1 5 10 15

Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
20 25 30

45 Glu Ser Val Ala Ser His Phe Ala Leu Val Thr Ala Tyr Glu Asp Ile
35 40 45

Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
50 55 60

50 Arg Ile Arg Phe Leu Glu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
65 70 75 80

55 Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala Tyr
85 90 95

Arg Glu Val Cys Ile Asp Arg Asp Asn Leu Lys Ser Lys Leu Asp Lys
100 105 110

60 Met Asn Lys Asp Asn Ser Glu Ser Leu Lys Val Leu Asn Glu Gln Leu

324

	115	120	125
	Gln Ser Lys Glu Val Glu Leu Leu Gln Leu Arg Thr Glu Val Glu Thr		
	130	135	140
5	Gln Gln Val Met Arg Asn Leu Asn Pro Pro Ser Ser Asn Trp Glu Val		
	145	150	155 160
10	Glu Lys Leu Ser Cys Asp Leu Lys Ile His Gly Leu Glu Gln Glu Leu		
	165	170	175
	Glu Leu Met Arg Lys Glu Cys Ser Asp Leu Lys Ile Glu Leu Gln Lys		
	180	185	190
15	Ala Lys Gln Thr Asp Pro Tyr Gln Glu Asp Asn Leu Lys Ser Arg Asp		
	195	200	205
	Leu Gln Lys Leu Ser Ile Ser Ser Asp Asn Met Gln His Ala Tyr Trp		
	210	215	220
20	Glu Leu Lys Arg Glu Met Ser Asn Leu His Leu Val Thr Gln Val Gln		
	225	230	235 240
	Ala Glu Leu Leu Arg Lys Leu Lys Thr Ser Thr Ala Ile Lys Lys Ala		
25	245	250	255
	Cys Ala Pro Val Gly Cys Ser Glu Asp Leu Gly Arg Asp Ser Thr Lys		
	260	265	270
30	Leu His Leu Met Asn Phe Thr Ala Thr Tyr Thr Arg His Pro Pro Leu		
	275	280	285
	Leu Pro Asn Gly Lys Ala Leu Cys His Thr Thr Ser Ser Pro Leu Pro		
	290	295	300
35	Gly Asp Val Lys Val Leu Ser Glu Lys Ala Ile Leu Gln Ser Trp Thr		
	305	310	315 320
	Asp Asn Glu Arg Ser Ile Pro Asn Asp Gly Thr Cys Phe Gln Glu His		
40	325	330	335
	Ser Ser Tyr Gly Arg Asn Ser Leu Glu Asp Asn Ser Trp Val Phe Pro		
	340	345	350
45	Ser Pro Pro Lys Ser Ser Glu Thr Ala Phe Gly Glu Thr Lys Thr Lys		
	355	360	365
	Thr Leu Pro Leu Pro Asn Leu Pro Pro Leu His Tyr Leu Asp Gln His		
	370	375	380
50	Asn Gln Asn Cys Leu Tyr Lys Asn		
	385	390	

55

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

60

325

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

5 Met His His His Thr Gln Leu Met Phe Ile Tyr Leu Phe Ile Tyr Leu
 1 5 10 15
 Phe Ile Leu Gly Val Phe Phe Phe Phe Phe Xaa
 20 25

10

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

20 Met Asn Cys Ile Leu Leu Leu Tyr Leu Leu Ile Pro Thr Ile Ser Ile
 1 5 10 15
 Ser Val Val Pro Tyr Val Ala Leu Asn Ile Lys Tyr Ile Lys Glu Cys
 20 25 30
 25 Thr Glu Asn Ser Phe Tyr Xaa
 35

30

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

40 Met Leu Leu His Leu Thr Ala Ala Phe Leu Gln Arg Ala Gln Phe Ser
 1 5 10 15
 Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
 20 25 30
 45 Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
 35 40 45
 Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
 50 55 60
 50 Arg Val Leu Phe Ile Tyr Xaa
 65 70

55

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

5 Met Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe
 1 5 10 15
 Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile
 20 25 30
 10 Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe
 35 40 45
 Ser Thr Tyr Phe Pro Ala Phe Met Asn Ser Leu Ser Arg Ser Lys Arg
 50 55 60
 15 Thr Pro Ala Gly Ser Glu Ser Arg Cys Arg Thr Gln Arg Asn Asn His
 65 70 75 80
 Leu Leu Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 214:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Met Ser Lys Arg Ser Ala Ser Phe Ile Leu Leu Pro Leu Leu Phe Leu
 1 5 10 15
 35 Lys Gly Ser Phe Ala Lys Leu Asn Ala Arg Ile Ser Asp Cys Leu Glu
 20 25 30
 Glu Arg Tyr Cys His Asn Leu Trp Met Val Phe Gln Gly Cys Val Ile
 35 40 45
 40 Thr Glu Leu His Leu Ser Arg Met Ser Lys Thr Leu Ser Ser Leu Cys
 50 55 60
 Tyr Asp Phe Val Ile Asn Val Tyr Ile Phe Phe Lys Phe Leu Asp Ile
 45 65 70 75 80
 Thr

50

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

60 Met Cys Ser Leu Phe Glu Ser Arg Phe Phe Cys Phe Val Leu Phe Ser

327

1 5 10 15

Glu Lys Ile Ile Gln Leu Cys Ala Ser Ile Ala Phe Leu Cys Phe Val
 20 25 30

Lys His Val Pro Trp Pro Lys Trp Lys Arg Lys Cys Leu Ile Asn Ala
 35 40 45

Phe

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

	Met	Thr	Leu	Arg	Pro	Ser	Leu	Leu	Pro	Leu	His	Leu	Leu	Leu	Leu	
	1				5					10						15
25	Leu	Leu	Ser	Ala	Ala	Val	Cys	Arg	Ala	Glu	Ala	Gly	Leu	Glu	Thr	Glu
				20					25					30		
	Ser	Pro	Val	Arg	Thr	Leu	Gln	Val	Glu	Thr	Leu	Val	Glu	Pro	Pro	Glu
			35					40					45			
30	Pro	Cys	Ala	Glu	Pro	Ala	Ala	Phe	Gly	Asp	Thr	Leu	His	Ile	His	Tyr
		50					55						60			
	Thr	Gly	Ser	Leu	Val	Asp	Gly	Arg	Ile	Ile	Asp	Thr	Ser	Leu	Thr	Arg
35	65					70					75					80
	Asp	Pro	Leu	Val	Ile	Glu	Leu	Gly	Gln	Lys	Gln	Val	Ile	Pro	Gly	Leu
				85						90					95	
40	Glu	Gln	Ser	Leu	Asp	Met	Cys	Val	Gly	Glu	Lys	Arg	Arg	Ala	Ile	
				100				105					110			
	Ile	Pro	Ser	His	Leu	Ala	Tyr	Gly	Lys	Arg	Gly	Phe	Pro	Pro	Ser	Val
			115					120					125			
45	Pro	Ala	Asp	Ala	Val	Val	Gln	Tyr	Asp	Val	Glu	Leu	Ile	Ala	Leu	Ile
		130					135					140				
	Arg	Ala	Asn	Tyr	Trp	Leu	Lys	Leu	Val	Lys	Gly	Ile	Leu	Pro	Leu	Val
50	145					150					155					160
	Gly	Met	Ala	Met	Val	Pro	Pro	Ser	Trp	Ala	Ser	Leu	Gly	Ile	Thr	Tyr
				165						170					175	
55	Thr	Glu	Arg	Pro	Ile	Asp	Pro	Lys	Ser	Pro	Lys	Arg	Ser	Ser	Arg	Lys
				180					185					190		
	Arg	Asn	Glu	Thr	Arg	Ala	Lys	Arg	Asn	Asn	Lys					
		195						200								

60

(2) INFORMATION FOR SEQ ID NO: 217:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 186 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

10 Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe
 1 5 10 15

15 Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Val Cys Glu
 20 25 30

Ser Pro Glu Ser Pro Ala Gln Pro Ser Gly Ser Ser Leu Pro Ala Trp
 35 40 45

20 Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp
 50 55 60

Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro
 65 70 75 80

25 His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly
 85 90 95

Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu
 100 105 110

30 Leu Thr Lys Ala Glu Lys His Val His Xaa Phe Met Met Asp Thr Gln
 115 120 125

35 Leu Thr Lys Arg Ile Lys Asn Xaa Ala Ala Asn Val Leu Xaa Glu Thr
 130 135 140

Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Lys Ile Asp His Ala
 145 150 155 160

40 Lys Val Arg Asn Thr Arg Gly Ser Ser Ser Lys Tyr Pro Pro Val Glu
 165 170 175

45 Glu Arg Gln Asp Gly Thr Glu Glu Ala Glu
 180 185

(2) INFORMATION FOR SEQ ID NO: 218:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
 1 5 10 15

60 Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro

329

20 25 30

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
35 40 45

5 Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
50 55 60

10 Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
65 70 75 80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
85 90

15

(2) INFORMATION FOR SEQ ID NO: 219:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

25 Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
1 5 10 15

Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
20 25 30

30 Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Glu Gln Glu Ser Gln
35 40 45

35 Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
50 55 60

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Glu Arg Lys Ile Asn
65 70 75 80

40 Lys Met Thr Asp Lys Leu Lys Thr His Val Lys Ala Arg Thr Ala Gln
85 90 95

Leu Ala Lys Ile Lys Trp Val Ile Ser Val Ala Phe Tyr Val Leu Gln
100 105 110

45 Ala Ala Leu Met Ile Ser Leu Ile Trp Lys Tyr Tyr Ser Val Pro Val
115 120 125

50 Ala Val Val Pro Ser Lys Trp Ile Thr Leu Xaa
130 135

55 (2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

330

Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
1 5 10 15

5 Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
20 25 30

Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Asp Arg Ser His Arg
35 40 45

10

15

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile
25 1 5 10 15

Val Phe Phe Ser Leu Gly Val Phe Cys Ile Cys His Ser His Trp Tyr
20 25 30

30 His Thr Leu Gln Gln Met Ala Gly Thr Glu Pro Lys Ala Leu Leu Leu
35 40 45

Ser Pro Pro Ala Ala Thr Thr Phe Val Thr Val Thr His Glu Val Trp
50 55 60

35

Lys Glu Gln Ala Leu Ala
65 70

40

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

Met Thr Cys Ser Val Ala Leu Leu Leu Ile Leu Gly Leu Arg Cys Ser
50 1 5 10 15

Gly Val Arg Pro Gly Leu Val Gly Glu Gly His Asn Pro Ser Leu Leu
20 25 30

55 Val Cys Leu Leu Leu Lys Asp Ser Arg Thr Asn Gln Gly Ser Cys Pro
35 40 45

Gly Gly Pro Trp Ser Glu Arg Asp Ile Glu Ser Val Thr Ser Asp Asn
50 55 60

60

Cys Glu Ala Thr Leu Gly Tyr Arg Asn His Ser Leu Pro Ser Asn Tyr
65 70 75 80

Tyr Asn Ser

5

(2) INFORMATION FOR SEQ ID NO: 223:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Met Leu Thr Arg Ser Leu Lys Thr Leu Pro Ser Ala Cys Thr Ala Phe
1 5 10 15

20

Leu Leu Leu Phe Phe Leu Phe Ser Ser Gly Asp Pro Glu Leu Ser Cys
20 25 30

Ser Cys Thr Leu Arg Thr Gln Ser Ser Trp Ser
35 40

25

(2) INFORMATION FOR SEQ ID NO: 224:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His Gly
1 5 10 15

40

Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly Arg
20 25 30

Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala His
35 40 45

45

Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val Ala
50 55 60

Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu Gly
65 70 75 80

50

Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp Val
85 90 95

Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg His
100 105 110

55

Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp Arg
115 120 125

60

Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Xaa Thr Tyr Gly His

332

130 135 140

Xaa Xaa Pro Xaa Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr Tyr
 145 150 155 160

5 Lys Lys Met Leu Xaa Arg Asp Glu Arg Arg Phe Arg Val Ala Asp Gln
 165 170 175

10 Asp Gly Asp Ser Met Ala Thr Arg
 180

(2) INFORMATION FOR SEQ ID NO: 225:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Met Trp Leu Phe Ile Leu Leu Ser Leu Ala Leu Ile Ser Asp Ala Met
 1 5 10 15

25 Val Met Asp Glu Lys Val Lys Arg Ser Leu Cys Trp Thr Arg Leu Leu
 20 25 30

Pro Ser Ala Thr Thr Met Pro Xaa Thr Arg Ile Thr Pro Asn Thr Gly
 35 40 45

30 Ala Glu Xaa Ile Ser Val Xaa Thr Ala Thr Ser Ser Pro Ser Pro Leu
 50 55 60

35 Thr Ala Pro Ile Met Trp Pro
 65 70

(2) INFORMATION FOR SEQ ID NO: 226:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Met His Val Phe Val Leu Glu Ile Phe Leu
 1 5 10

50

(2) INFORMATION FOR SEQ ID NO: 227:

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

60 Met Ala Val Ala Thr Leu Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu

333

1 5 10 15
 Thr Phe Ile Thr Asp Asn Ser Leu Val Ala Ala Gly His Asp Cys Phe
 20 25 30
 5 Pro Val Leu Phe Thr Tyr Asp Ala Ala Ala Gly Met Leu Ser Phe Gly
 35 40 45
 10 Gly Arg Leu Asp Val Pro Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala
 50 55 60
 Arg Glu Arg Phe Gln Asn Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly
 65 70 75 80
 15 Thr Ala Ala Gly Ala Gly Leu Asp Ser Leu His Lys Asn Ser Val Ser
 85 90 95
 Gln Ile Ser Val Leu Ser Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys
 100 105 110
 20 Thr Thr Gly Met Asp Gly Gly Met Ser Ile Trp Asp Val Lys Ser Leu
 115 120 125
 25 Glu Ser Ala Leu Lys Asp Leu Lys Ile Lys
 130 135

30 (2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Leu Gly Ser Leu Ser Thr Ala Pro Ser Ser Ala Leu Pro Thr Leu Gly
 1 5 10 15
 40 Ala Arg Arg Thr Arg Ser Lys
 20

45 (2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Met Thr Tyr Phe Ser Gly Leu Leu Val Ile Leu Ala Phe Ala Ala Trp
 1 5 10 15
 55 Val Ala Leu Ala Glu Gly Leu Gly Val Ala Val Tyr Ala Ala Ala Val
 20 25 30
 60 Leu Leu Gly Ala Gly Cys Ala Thr Ile Leu Val Thr Ser Leu Ala Met
 35 40 45

334

Thr Ala Asp Leu Ile Gly Pro His Thr Asn Ser Gly Ala Phe Val Tyr
 50 55 60

5 Gly Ser Met Ser Phe Leu Asp Lys Val Ala Asn Gly Leu Ala Val Met
 65 70 75 80

Ala Ile Gln Ser Leu His Pro Cys Pro Ser Glu Leu Cys Cys Arg Ala
 85 90 95

10 Cys Val Ser Phe Tyr His Trp Ala Met Val Ala Val Thr Gly Gly Val
 100 105 110

Gly Val Ala Ala Ala Leu Cys Leu Cys Ser Leu Leu Trp Pro Thr
 15 115 120 125

Arg Leu Arg Arg Xaa
 130

20

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

30 Gly Lys Pro Thr Gly Lys Ser Leu Pro Leu Met Trp Met Ile Leu Met
 1 5 10 15

Gln Pro Ile Ile Met Ile Ser Met Met Ser Asn Gly
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 231:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

45

Met Gln Gly Lys Phe Met Lys Val Gln Val Tyr Arg Phe Leu Lys Tyr
 1 5 10 15

50

Leu Leu Met Leu Leu Cys Met Phe Val Asn Arg Gly Met Ser Lys Asp
 20 25 30

Ser Thr Lys Lys Pro Gly Gln Glu Lys Leu Lys Val Ser Leu Gly Ser
 35 40 45

55

Ile Leu Asn Met Lys Ser Gln Arg Pro Leu Ser Trp Cys
 50 55 60

60

(2) INFORMATION FOR SEQ ID NO: 232:

335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Met Met Glu Arg Ser Met Met Ile Leu Leu Met Ala Ala Ser Met Thr
 1 5 10 15

Met Thr Ser Thr Gln Leu Trp Ser Phe Cys Cys Val His
 20 25

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Met Trp Tyr Gln Leu Ala Lys Glu Glu Pro Gly Val Gly Ala Cys Ala
 1 5 10 15

Leu Asp

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Leu Xaa
 1

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Met Leu Ile Cys Arg Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn
 1 5 10 15

Phe Met Val Arg Leu Phe Val Val Ile Val Met Phe Ala Trp Ser Ile
 20 25 30

Val Ala Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg
 35 40 45

336

Ala Leu Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp
 50 55 60

5 Met Ile Leu Thr Phe Thr Pro Gln
 65 70

10 (2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Met Arg Ser Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15

20

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
 20 25 30

25

Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Xaa Pro
 35 40 45

Ala Trp Pro Ser Ala Cys Thr Arg Pro Trp Pro Arg Thr Arg Gln Trp
 50 55 60

30

Arg Thr Ser Trp Cys His Pro Trp Trp Trp Pro Arg Arg Trp Gly Ser
 65 70 75 80

Cys Arg Trp Ala Ala Arg Arg Pro Arg Arg Arg Pro Arg Gln Cys
 85 90 95

35

40

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Met Arg Ser Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15

50

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
 20 25 30

55

Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Lys Arg
 35 40 45

Pro Gly Leu Gln Leu Val Pro Gly His Gly Gln Gly Pro Gly Ser Gly
 50 55 60

60

337

Glu His Pro Gly Val Thr Arg Gly Gly Gly Leu Val Ala Gly Ala Arg
65 70 75 80

5 Val Ala Gly Arg Gln Gly Asp His Gly Val Ala Gly Gln Gly Ser Ala
85 90 95

Glu Arg Arg Ala Ala Ala Arg Arg Gly Gly Ala Arg Arg Pro Gly Arg
100 105 110

10 Ala Ala Ala Leu Thr Gln Gln Leu His Gly Ala Gln Arg Asp Leu Glu
115 120 125

Ala Gly Gln Pro Thr Val Arg Thr Gln Leu Ser Glu Leu Arg Xaa
130 135 140

15

(2) INFORMATION FOR SEQ ID NO: 238:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

25

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
1 5 10 15

30

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
20 25 30

Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Xaa Arg
35 40 45

35

Pro Gly Leu Gln Leu Val Pro Gly His Gly Gln Gly Pro Gly Ser Gly
50 55 60

Glu His Pro Gly Val Thr Arg Gly Gly Gly Leu Val Ala Gly Ala Arg
65 70 75 80

40

Val Ala Gly Arg Gln Gly Asp His Gly Val Ala Gly Gln Gly Ser Ala
85 90 95

Glu Arg Arg Ala Ala Ala Arg Arg Gly Gly Ala Arg Arg Pro Gly Arg
100 105 110

45

Ala Ala Ala Leu Thr Gln Gln Leu Xaa Gly Ala Gln Arg Asp Leu Glu
115 120 125

50

Ala Gly Gln Pro Thr Val Arg Thr Gln Leu Ser Glu Leu Arg
130 135 140

55

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

5 Asp Pro Glu Ala Ala Asp Ser Gly Glu Pro Gln Asn Lys Arg Thr Pro
 1 5 10 15
 Asp Leu Pro Glu Glu Glu Tyr Val Lys Glu Glu Ile Gln Glu Asn Glu
 20 25 30
 10 Glu Ala Val Lys Lys Met Leu Val Glu Ala Thr Arg Glu Phe Glu Glu
 35 40 45
 Val Val Val Asp Glu Ser
 50

15

(2) INFORMATION FOR SEQ ID NO: 240:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

25 Gln Lys Leu Lys Arg Lys Ala Glu Glu Asp Pro Glu Ala Ala Asp Ser
 1 5 10 15
 Gly Glu Pro Gln Asn Lys Arg Thr Pro Asp Leu Pro Glu Glu Glu Tyr
 20 25 30
 30 Val Lys Glu Glu Ile Gln Glu Asn Glu Glu Ala Val Lys Lys Met Leu
 35 40 45
 Val Glu Ala Thr Arg Glu Phe Glu Glu Val Val Val Asp Glu Ser
 35 50 55 60

(2) INFORMATION FOR SEQ ID NO: 241:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

45 Lys Ala Met Glu Lys Ser Ser Leu Thr Gln His Ser Trp Gln Ser Leu
 1 5 10 15
 50 Lys Asp Arg Tyr Leu Lys His Leu Arg Gly Gln Glu His Lys Tyr Leu
 20 25 30
 Leu Gly Asp Ala Pro Val Ser Pro Ser Ser Gln Lys Leu Lys Arg Lys
 35 40 45
 55 Ala Glu Glu Asp Pro Glu Ala Ala Asp Ser Gly Glu Pro Gln Asn Lys
 50 55 60
 60 Arg Thr Pro Asp Leu Pro Glu Glu Glu Tyr Val Lys Glu Glu Ile Gln
 65 70 75 80

339

Glu Asn Glu Glu Ala Val Lys Lys Met Leu Val Glu Ala Thr Arg Glu
85 90 95

5 Phe Glu Glu Val Val Val Asp Glu Ser Pro Pro Asp Phe Glu Ile His
100 105 110

Ile

10

(2) INFORMATION FOR SEQ ID NO: 242:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

20

Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile
1 5 10 15

25

Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe
20 25 30

Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met Leu
35 40 45

30

Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser
50 55 60

Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly
65 70 75 80

35

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr
85 90 95

40

Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe
100 105 110

Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala
115 120 125

45

Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg
130 135 140

Val Leu Phe Ile
145

50

(2) INFORMATION FOR SEQ ID NO: 243:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

60

340

Ala Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys
 1 5 10 15

5 Trp Ile Leu Ile Val Arg Phe Ser
 20

10 (2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Met Lys His Leu Ser Ala Trp Asn Phe Thr Lys Leu Thr Phe Leu Gln
 1 5 10 15
 20 Leu Trp Glu Ile Phe Glu Gly Ser Val Glu Asn Cys Gln Thr Leu Thr
 20 25 30
 Ser Tyr Ser Lys Leu Gln Ile Lys Tyr Thr Phe Ser Arg Gly Ser Thr
 35 40 45
 25 Phe Tyr Ile
 50

30 (2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Phe Ser Ser Asp Phe Arg Thr Ser Pro Trp Glu Ser Arg Arg Val Glu
 40 1 5 10 15
 Ser Lys Ala Thr Ser Ala Arg Cys Gly Leu Trp Gly Ser Gly Pro Arg
 20 25 30
 45 Arg Arg Pro Ala Ser Gly Met Phe Arg Gly Leu Ser Ser Trp Leu Gly
 35 40 45
 Leu Gln Gln Pro Val Ala Gly Gly Gly Gln Pro Asn Gly Asp Ala Pro
 50 50 55 60
 Pro Glu Gln Pro Ser Glu Thr Val Ala Glu Ser Ala Glu Glu Glu Leu
 65 70 75 80
 55 Gln Gln Ala Gly Asp Gln Glu Leu Leu His Gln Ala Lys Asp Phe Gly
 85 90 95
 Asn Tyr Leu Phe Asn Phe Ala Ser Ala Ala Thr Lys Lys Ile Thr Glu
 100 105 110
 60 Ser Val Ala Glu Thr Ala Gln Thr Ile Lys Lys Ser Val Glu Glu Gly

341

115 120 125

Lys Ile Asp Gly Ile Ile Asp Lys Thr Ile Ile Gly Asp Phe Gln Lys
130 135 140

5 Glu Gln Lys Lys Phe Val Glu Glu Gln His Thr Lys Lys Ser Glu Ala
145 150 155 160

10 Ala Val Pro Pro Trp Val Asp Thr Asn Asp Glu Glu Thr Ile Gln Gln
165 170 175

Gln Ile Leu Ala Leu Ser Ala Asp Lys Arg Asn Phe Leu Arg Asp Pro
180 185 190

15 Pro Ala Gly Val Gln Phe Asn Phe Asp Phe Asp Gln Met Tyr Pro Val
195 200 205

Ala Leu Val Met Leu
210

20

(2) INFORMATION FOR SEQ ID NO: 246:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

30

Met Arg Phe Ala Leu Val Pro Lys Leu Val Lys Glu Glu Val Phe Trp
1 5 10 15

35

Arg Asn Tyr Phe Tyr Arg Val Ser Leu Ile Lys Gln Ser Ala Gln Leu
20 25 30

Thr Ala Leu Ala Ala Gln Gln Gln Ala Ala Gly Lys Gly Gly Glu Glu
35 40 45

40 Gln

45

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

50

Ser Thr Ser Pro Gly Val Ser Glu Phe Val Ser Asp Ala Phe Asp Ala
1 5 10 15

55

Cys Asn Leu Asn Gln Glu Asp Leu Arg Lys Glu Met Glu Gln Leu Val
20 25 30

60

Leu Asp Lys Lys Gln Glu Glu Thr Ala Val Leu Glu Glu Asp Ser Ala
35 40 45

342

Asp Trp Glu Lys Glu Leu Gln Gln Glu Leu Gln Glu Tyr Glu Val Val
 50 55 60

5 Thr Glu Ser Glu Lys Arg Asp Glu Asn Trp Asp Lys
 65 70 75

10 (2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

20 Ser Pro Trp Glu Ser Arg Arg Val Glu Ser Lys Ala Thr Ser Ala Arg
 1 5 10 15

Cys Gly Leu Trp Gly Ser Gly Pro Arg Arg Arg Pro Ala Ser Gly Met
 20 25 30

25 Phe Arg Gly Leu Ser Ser Trp Leu Gly Leu Gln Gln Pro Val Ala Gly
 35 40 45

Gly Gly Gln Pro Asn Gly Asp Ala Pro Pro Glu Gln Pro Ser
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

40 Pro Val Ala Gly Gly Gly Gln Pro Asn Gly Asp Ala Pro Pro Glu Gln
 1 5 10 15

Pro Ser Glu Thr Val Ala Glu Ser Ala Glu Glu Glu Leu Gln Ala
 20 25 30

45

Gly Asp Gln Glu Leu Leu His Gln Ala Lys Asp Phe Gly Asn Tyr Leu
 35 40 45

50 Phe Asn Phe Ala Ser Ala Ala Thr Lys Lys Ile Thr Glu Ser Val Ala
 50 55 60

Glu
 65

55

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 72 amino acids

343

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

5 Phe Gln Lys Glu Gln Lys Lys Phe Val Glu Glu Gln His Thr Lys Lys
 1 5 10 15
 Ser Glu Ala Ala Val Pro Pro Trp Val Asp Thr Asn Asp Glu Glu Thr
 20 25 30
 10 Ile Gln Gln Gln Ile Leu Ala Leu Ser Ala Asp Lys Arg Asn Phe Leu
 35 40 45
 Arg Asp Pro Pro Ala Gly Val Gln Phe Asn Phe Asp Phe Asp Gln Met
 15 50 55 60
 Tyr Pro Val Ala Leu Val Met Leu
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

30 Pro Phe Ile Cys Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser
 1 5 10 15
 Pro Ile Leu Ala Arg Lys Leu Cys Glu Gly Ala Ala
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 252:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

45

Lys Glu Asp Pro Ala Asn Thr Val Tyr Ser Thr Val Glu Ile Pro Lys
 1 5 10 15

50

Lys Met Glu Asn Pro His Ser Leu Leu Thr Met Pro Asp Thr Pro Arg
 20 25 30

Leu

55

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 227 amino acids

344

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

5 Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu Ala Gln
 1 5 10 15
 Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp Val Thr
 20 25 30
 10 Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly Lys Phe
 35 40 45
 Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val Ala Ser
 15 50 55 60
 Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu Asp Phe
 65 70 75 80
 20 Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val Ile Arg
 85 90 95
 Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly Gly Gln
 100 105 110
 25 Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu Gly Gln
 115 120 125
 Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val Gly Met
 30 130 135 140
 Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg Val Met
 145 150 155 160
 35 Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser Leu Pro
 165 170 175
 Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro Ser Arg
 180 185 190
 40 Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile Ile Glu
 195 200 205
 Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala Ile Arg
 45 210 215 220
 Met Gln Pro
 225

50

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

60 Ser Val Ala Ala Phe Glu Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala

345

1 5 10 15
 Ser Lys Gly Gly Ile Val Gly Met Thr Leu Pro Ile Ala
 20 25

5

(2) INFORMATION FOR SEQ ID NO: 255:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

15

Ala Arg Arg Ser Gly Ala Glu Leu Ala Trp Asp Tyr Leu Cys Arg Trp
 1 5 10 15

20

Ala Gln Lys His Lys Asn Trp Arg Phe Gln Lys Thr Arg Gln Thr Trp
 20 25 30

Leu Leu Leu His Met Tyr Asp Ser Asp Lys Val Pro Asp Glu His Phe
 35 40 45

25

Ser Thr Leu Leu Ala Tyr Leu Glu Gly Leu Gln Gly Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 256:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

His Pro Ile Glu Trp Ala Ile Asn Ala Ala Thr Leu Ser Gln Phe Tyr
 1 5 10 15

40

Ile Asn Lys Leu Cys Phe
 20

(2) INFORMATION FOR SEQ ID NO: 257:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Cys Trp Ile Lys Tyr Cys Leu Thr Leu Met Gln Asn Ala Gln Leu Ser
 1 5 10 15

55

Met Gln Asp Asn Ile Gly
 20

60

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

5
 10 Lys Val Ser Tyr Leu Arg Pro Leu Asp Phe Glu Glu Ala Arg Glu Leu
 1 5 10 15
 Phe Leu Leu Gly Gln His Tyr Val Phe
 20 25

15

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

20
 25 Met Glu Arg Arg Cys Lys Met His Lys Arg Xaa Ile Ala Met Leu Glu
 1 5 10 15
 Pro Leu Thr Val Asp Leu Asn Pro Gln
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

35
 40 Ser His Ile Val Lys Lys Ile Asn Asn Leu Asn Lys Ser Ala Leu Lys
 1 5 10 15
 Tyr Tyr Gln Leu Phe Leu Asp
 45 20

45

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

50
 55 Phe Thr His Leu Ser Thr Cys Leu Leu Ser Leu Leu Leu Val Arg Met
 1 5 10 15
 60 Ser Gly Phe Leu Leu Leu Ala Arg Ala Ser Pro Ser Ile Cys Ala Leu

60

347

20 25 30

Asp Ser Ser Cys Phe Val Gln Glu Tyr Cys Ser Ser Tyr Ser Ser Ser
35 40 45

5 Cys Phe Leu His Gln His Phe Pro Ser Leu Leu Asp His Leu Cys Gln
50 55 60

10

(2) INFORMATION FOR SEQ ID NO: 262:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Phe Leu Leu Leu Ala Arg Ala Ser Pro Ser Ile Cys Ala Leu Asp Ser
1 5 10 15

25

Ser Cys Phe Val Gln Glu Tyr
20

30

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Pro Asp Gly Arg Val Thr Asn Ile Pro Gln Gly Met Val Thr Asp Gln
1 5 10 15

40

Phe Gly Met Ile Gly Leu Leu Thr Phe Ile Arg Ala Ala Glu Thr Asp
20 25 30

45

Pro Gly Met Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr Leu Gly
35 40 45

Leu Asn Leu Asn Ser
50

50

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

60

Glu Asp Leu Leu Phe Tyr Leu Tyr Tyr Met Asn Gly Gly Asp Val Leu

348

1 5 10 15
 Gln Leu Leu Ala Ala Val Glu Leu Phe Asn Arg Asp Trp Arg Tyr His
 20 25 30
 5 Lys Glu Glu Arg Val Trp Ile Thr Arg
 35 40

10 (2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 15 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

20 Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr Leu Gly Leu Asn Leu
 1 5 10 15
 Asn Ser Pro Glu Asn Leu Tyr Pro
 20

25 (2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 30 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

35 His Asn Glu Asp Phe Pro Ala Leu Pro Gly Ser
 1 5 10

40 (2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 amino acids
 45 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu
 1 5 10 15
 50 Leu Gly Gln Lys Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp
 20 25 30

55 Met Cys Val Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala
 35 40 45

Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val
 50 55 60

60 Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg

349

65

70

75

5 (2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser
1 5 10 15

15

20

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

Cys Glu Ser Pro Glu Ser Pro Ala Gln Pro Ser Gly Ser Ser Leu Pro
1 5 10 15

30

Ala Trp Tyr His
20

35

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Glu Glu Ala Gly Ala Gly Arg Arg Cys Ser His Gly Gly Ala Arg Pro
1 5 10 15

45

Ala Gly Leu Gly Asn Glu Gly Leu Gly Leu Gly Gly Asp Pro Asp His
20 25 30

50

Thr Asp Thr Gly Ser Arg Ser Lys Gln Arg Ile Asn Asn Trp Lys Glu
35 40 45

Ser Lys His Lys Val Ile Met Ala Ser Ala Ser Ala Arg Gly Asn Gln
50 55 60

55

Asp Lys Asp Ala His Phe Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe
65 70 75 80

60

Cys Pro Lys Ser Lys Leu His Ile His Arg Ala Glu Ile Ser Lys

350

85

90

95

5 (2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

Ser Lys Gln Arg Ile Asn Asn Trp Lys Glu Ser Lys His Lys Val Ile
1 5 10 15

15

Met Ala Ser Ala Ser Ala Arg
20

20

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro Arg
1 5 10 15

30

Asn Thr Ala Xaa Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly Pro Ser
20 25 30

35

40 (2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Phe Tyr Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr
1 5 10 15

50

Lys Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His
20 25 30

55

Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn Glu
35 40 45

Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr Lys Ala
50 55 60

60

Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro Thr Leu Ala

351

	65					70						75					80
	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	Pro	Val	Gly	Thr	
					85					90					95		
5	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	Tyr	Leu	Ile	Val	Gly	
				100					105					110			
	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	Val	Thr	Phe	Ile	Pro	Phe	
10			115					120					125				
	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	Lys	His	Thr	Thr	Asp	Leu	Gly	
		130					135					140					
15	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	
	145					150					155					160	
	Leu	Gly	Gly	Leu	Pro	Gly	His	Gln	Ala	Val	Asp	Ser	Pro	Thr	Ser	Val	
					165					170					175		
20	Ala	Ser	Val	Asp	Gly	Pro	Val	Leu	Met								
				180					185								

25 (2) INFORMATION FOR SEQ ID NO: 274:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

35	Tyr Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys 1 5 10 15
	Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His Leu 20 25 30
40	Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn Glu Gly 35 40 45
	Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr Lys Ala Arg 50 55 60
45	Lys Ser 65

50

(2) INFORMATION FOR SEQ ID NO: 275:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

60 Asn Val Arg Ala Leu Leu His Arg Met Pro Glu Pro Pro Lys Ile Asn
1 5 10 15

352

Thr Ala Lys Phe Asn Asn Asn Lys Arg Lys Asn Leu Ser Leu
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

15 Asn Thr Asn Gln Arg Glu Ala Leu Gln Tyr Ala Lys Asn Phe Gln Pro
 1 5 10 15
 Phe Ala Leu Asn His Gln Lys Asp Ile Gln Val Leu Met Gly Ser Leu
 20 20 25 30
 Val Tyr Leu Arg Gln Gly Ile Glu Asn Ser Pro Tyr Val His Leu Leu
 35 40 45
 25 Asp Ala Asn Gln Trp Ala Asp Ile Cys Asp Ile Phe Thr Arg Asp Ala
 50 55 60
 Cys Ala Leu Leu Gly Leu Ser Val Glu Ser Pro Leu Ser Val Ser Phe
 65 70 75 80
 30 Ser Ala Gly Cys Val Ala Leu Pro Ala Leu Ile Asn Ile Lys Ala Val
 85 90 95
 Ile Glu Gln Arg Gln Cys Thr Gly Val Trp Asn Gln Lys Asp Glu Leu
 100 105 110
 35 Pro Ile Glu Val Asp Leu Gly Lys Lys Cys Trp Tyr His Ser Ile Phe
 115 120 125
 40 Ala Cys Pro Ile Leu Arg Gln Gln Thr Thr Asp Asn Asn Pro Pro Met
 130 135 140
 Lys Leu Val Cys Gly His Ile Ile Ser Arg Asp Ala Leu Asn Lys Met
 145 150 155 160
 45 Phe Asn Gly Ser Lys Leu Lys Cys Pro Tyr Cys Pro Met Glu Gln Ser
 165 170 175
 Pro Gly Asp Ala Lys Gln Ile Phe Phe
 180 185

50

(2) INFORMATION FOR SEQ ID NO: 277:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

60

353

Ser Tyr Leu Ser Ala Cys Phe Ala Gly Cys Asn Ser Thr Asn Leu Thr
 1 5 10 15
 Gly Cys Ala Cys Leu Thr Thr Val Pro Ala Glu Asn Ala Thr Val Val
 5 20 25 30
 Pro Gly Lys Cys Pro Ser Pro Gly Cys Gln Glu Ala Phe Leu Thr Phe
 35 40 45
 10 Leu Cys Val Met Cys Ile Cys Ser Leu Ile Gly Ala Met Ala Arg His
 50 55 60
 Pro
 65
 15

(2) INFORMATION FOR SEQ ID NO: 278:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:
 25

Pro Ser Val Ile Ile Leu Ile Arg Thr Val Ser Pro Glu Leu Lys Ser
 1 5 10 15
 Tyr Ala Leu Gly Val Leu Phe Leu Leu Leu Arg Leu Leu Gly Phe Ile
 30 20 25 30
 Pro Pro Pro Leu Ile Phe Gly Ala Gly Ile Asp Ser Thr Cys Leu Phe
 35 40 45
 35 Trp Ser Thr Phe Cys Gly Glu Gln Gly Ala Cys Val Leu Tyr Asp Asn
 50 55 60
 Val Val Tyr Arg Tyr Leu Tyr Val Ser Ile Ala Ile Ala Leu Lys Ser
 65 70 75 80
 40 Phe Ala Phe Ile

45

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:
 50

55 Gln Ser Leu Phe Thr Arg Phe Val Arg Val Gly Val Pro Thr Val Asp
 1 5 10 15
 Leu Asp Ala Gln Gly Arg Ala Arg Ala Ser Leu Cys Xaa Xaa Tyr Asn
 20 25 30
 60 Trp Arg Tyr Lys Asn Leu Gly Asn Leu Pro His Val Gln Leu Leu Pro

354

30

(2) INFORMATION FOR SEQ ID NO: 280:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

40 Leu Val Lys Glu Ala Lys Ile Ile Ala Met Thr Cys Thr His Ala Ala
1 5 10 15

Leu Lys Arg His Asp Leu Val Lys Leu Gly Phe Lys Tyr Asp Asn Ile
20 25 30

45 Leu Met Glu Glu Ala Ala Gln Ile Leu Glu Ile Glu Thr Phe Ile Pro
35 40 45

Leu Leu Leu Gln Asn Pro Gln Asp Gly Phe Ser Arg Leu Lys Arg Trp
50 55 60

Ile Met Ile Gly Asp His His Gln Leu Pro Pro Val Ile
65 70 75

55

(2) INFORMATION FOR SEQ ID NO: 281:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids

355

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

5 Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Xaa
 1 5 10 15

Xaa Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg
 20 25 30

10 Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Xaa Ala Ile Val Arg Asn
 35 40 45

15 Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu
 50 55 60

Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile
 65 70 75 80

20 Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser
 85 90 95

Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys
 100 105 110

25 Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu
 115 120 125

30

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

40 Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val Gly Thr
 1 5 10 15

Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Ala Met Val Met Thr
 20 25 30

45 Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly Ala Leu
 35 40 45

Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln Val His
 50 55 60

50 Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp Gly Leu
 65 70 75 80

Ala Ile Trp Tyr Thr
 85

55

60

(2) INFORMATION FOR SEQ ID NO: 283:

356

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

Pro Gly Thr Leu Gln Cys Ser Ala Leu His His Asp Pro Gly Cys Ala
 1 5 10 15

10 Asn Cys Ser Arg Phe Cys Arg Asp Cys Ser Pro Pro Ala Cys Gln Cys
 20 25 30

15

(2) INFORMATION FOR SEQ ID NO: 284:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

Phe Leu Tyr Asp Val Leu Met Xaa His Glu Ala Val Met Arg Thr His
 1 5 10 15

30 Gln Ile Gln Leu Pro Asp Pro Glu Phe Pro Ser
 20 25

35 (2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

Gly Trp Tyr Trp Cys Gly
 1 5

45

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

55 Met Lys Val Gly Ala Arg Ile Arg Val Lys Met Ser Val Asn Lys Ala
 1 5 10 15

His Pro Val Val Ser Thr His Trp Arg Trp Pro Ala Glu Trp Pro Gln
 20 25 30

60

357

Met Phe Leu His Leu Ala Gln Glu Pro Arg Thr Glu Val Lys Ser Arg
 35 40 45

5 Pro Leu Gly Leu Ala Gly Phe Ile Arg Gln Asp Ser Lys Thr Arg Lys
 50 55 60

Pro Leu Glu Gln Glu Thr Ile Met Ser Ala Ala Asp Thr Ala Leu Trp
 65 70 75 80

10 Pro Tyr Gly His Gly Asn Arg Glu His Gln Glu Asn Glu Leu Gln Lys
 85 90 95

Tyr Leu Gln Tyr Lys Asp Met His Leu Leu Asp Ser Gly Gln Ser Leu
 100 105 110

15 Gly His Thr His Thr Leu Gln Gly Ser His Asn Leu Thr Ala Leu Asn
 115 120 125

20 Ile
 -

(2) INFORMATION FOR SEQ ID NO: 287:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser Gly Gly
 1 5 10 15

35 Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly Gly Met
 20 25 30

Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp Leu Lys
 35 40 45

40

Ile

45

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

50

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

55 Glu Ala Ser Lys Ser Ser His Ala Gly Leu Asp Leu Phe Ser Val Ala
 1 5 10 15

Ala Cys His Arg Phe
 20

60

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

5
10 Tyr Met Gly Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe
1 5 10 15
Glu Arg Ser Phe Thr
20

15

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

20
25 Val Thr Gly Ile Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg
1 5 10 15
Val Gly Leu Leu Gln Tyr Ser Thr Gln Val His
30 20 25

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

35
40 Thr Glu Phe Thr Leu Arg Asn Phe Asn Ser Ala Lys Asp Met Lys Lys
1 5 10 15
45 Ala Val Ala His Met Lys Tyr Met
20

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

50
55 Gly Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg
1 5 10 15
60

359

Ser Phe Thr Gln Gly Glu Gly Ala Arg Pro Phe
 20 25

5

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

15

Ser Thr Arg Val Pro Arg Ala Ala Ile Val Phe Thr Asp Gly Arg Ala
 1 5 10 15

Gln Asp Asp Val Ser Glu Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile
 20 25 30

20

Thr Met Tyr Ala Val Gly Val Gly Lys Ala Ile Glu
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

30

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

35

Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro Thr Asn Lys His Leu Phe
 1 5 10 15

Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu Ile Ser Glu Lys Leu Lys
 20 25 30

40

Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 35 40

45

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Thr Gln Arg Leu Glu Glu Met Thr Gln Arg Met
 1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 10 amino acids

360

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

5 Pro Gln Gly Cys Pro Glu Gln Pro Leu His
 1 5 10

10 (2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Arg Cys Lys Lys Cys Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile
 1 5 10 15
 20 Asp Gly Ser Lys Ser Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln
 20 25 30
 25 Phe

30 (2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Met Ala Ala Leu Leu Leu Arg His Val Gly Arg His Cys Leu Arg Ala
 1 5 10 15
 40 His Phe Ser Pro Gln Leu Cys Ile Arg Asn Ala Val Pro Leu Gly Thr
 20 25 30
 Thr Ala Lys Glu Glu Met Glu Arg Phe Trp Asn Lys Asn Ile Gly Ser
 35 40 45
 45 Asn Arg Pro Leu Ser Pro His Ile Thr Ile Tyr Ser
 50 55 60

50 (2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

60 Val Phe Pro Leu Met Tyr His Thr Trp Asn Gly Ile Arg His Leu Met
 1 5 10 15

Trp Asp Leu Gly Lys Gly Leu Lys Ile Pro Gln Leu Tyr Gln Ser Gly
20 25 30

5

10 (2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ala Ala Leu Leu Arg His Val Gly Arg His Cys Leu Arg Ala
1 5 10 15

20

His

25

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

30 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Val Lys Ser Leu Cys Leu Gly Pro Ala Leu Ile His Thr Ala Lys Phe
1 5 10 15

35

Ala Leu

40

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

Val Phe Pro Leu Met Tyr His Thr Trp Asn Gly Ile Arg His Leu Met
1 5 10 15

50

Trp Asp Leu Gly Lys Gly Leu
20

55

(2) INFORMATION FOR SEQ ID NO: 303:

60 (i) SEQUENCE CHARACTERISTICS:

362

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

5

Arg Val Trp Asp Val Arg Pro Phe Ala Pro Lys Glu Arg Cys Val Lys
 1 5 10 15

10

Ile Phe Gln Gly Asn Val
 20

(2) INFORMATION FOR SEQ ID NO: 304:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

His Asn Phe Glu Lys Asn Leu Leu Arg Cys Ser Trp Ser Pro Asp Gly
 1 5 10 15

25

Ser Lys Ile Ala Ala Gly Ser Ala Asp Arg Phe Val Tyr Val
 20 25 30

30

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

Trp Asp Thr Thr Ser Arg Arg Ile Leu Tyr Lys Leu Pro Gly His Ala
 1 5 10 15

40

Gly Ser Ile Asn Glu Val Ala Phe His Pro Asp Glu Pro Ile
 20 25 30

45

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

55

Val Arg Gly Arg Thr Val Leu Arg Pro Gly Leu Asp Ala Glu Pro Glu
 1 5 10 15

Leu Ser Pro Glu
 20

60

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

10 Glu Gln Arg Val Leu Glu Arg Lys Leu Lys Lys Glu Arg Lys Lys Glu
1 5 10 15

Glu Arg Gln

15

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

25 Arg Leu Arg Glu Ala Gly Leu Val Ala Gln His Pro Pro
1 5 10

30

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

40 Gly Arg Ile Pro Ala Pro Ala Pro Ser Val Pro Ala Gly Pro Asp Ser
1 5 10 15

Arg

45

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

55 Thr Gly Cys Val Leu Val Leu Ser Arg Asn Phe Val Gln Tyr Ala Cys
1 5 10 15

Phe Gly Leu Phe Gly Ile Ile Ala Leu Gln Thr Ile Ala Tyr Ser Ile
20 25 30

60

364

Leu Trp Asp Leu Lys Phe Leu Met Arg Asn
 35 40

5

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Ser Arg Ser Glu Gly Lys Ser Met Phe Ala Gly Val Pro Thr Met Arg
 1 5 10 15

Glu Ser Ser Pro Lys Gln Tyr Met Gln Leu Gly Gly Arg Val Leu Leu
 20 25 30

20 Val Leu Met Phe Met Thr Leu Leu His Phe Asp Ala Ser Phe Phe Ser
 35 40 45

Ile Val Gln Asn Ile Val Gly
 50 55

25

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

35 Gly Thr Ala Glu Asp Phe Ala Asp Gln Phe Leu Arg Val Thr Lys Gln
 1 5 10 15

40 Tyr Leu Pro His Val Ala Arg Leu Cys Leu Ile Ser Thr Phe Leu Glu
 20 25 30

Asp Gly Ile Arg Met Trp Phe Gln Trp Ser Glu Gln Arg Asp Tyr Ile
 35 40 45

45 Asp Thr Thr Trp Asn Cys Gly Tyr Leu Leu Ala Ser
 50 55 60

50 (2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Ala Ser Phe Leu Leu Ser Arg Thr Ser Trp Gly Thr Ala Leu Met Ile
 1 5 10 15

60

365

Leu

5

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

10

Leu Met Arg Asn Glu Ser Arg Ser

15

1

5

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

20

Ala Ser Phe Leu Leu Ser Arg Thr Ser Trp Gly Thr Ala

25

1

5

10

30

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

35

Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met

40

1

5

10

15

Met Ser Ser Phe

20

45

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

50

Asp Pro Arg Arg Pro Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser

55

1

5

10

15

Glu Cys Asn Pro Ala Leu Asp Asp Pro Thr Pro

60

20

25

5 (2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met
1 5 10 15

15 Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser
20 25 30

20 (2)-INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu Gln Asn Pro Gln
1 5 10 15

30 Pro Met Thr Pro Pro Trp
20

35

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

40 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

45 Ala Ala Gly Asp Gly Asp Val Lys Leu Gly Thr Leu Gly Ser Gly Ser
1 5 10 15

Glu Ser Ser Asn Asp Gly Gly Ser Glu Ser Pro Gly Asp Ala Gly Ala
20 25 30

50 Ala Ala Xaa Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala Leu Leu Thr
35 40 45

Gly Gly Gly Glu
50

55

(2) INFORMATION FOR SEQ ID NO: 321:

60 (i) SEQUENCE CHARACTERISTICS:

367

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

5
Ala Ala Asp Asn Tyr Gly Ile Pro Arg Ala Cys Arg Asn Ser Ala Arg
1 5 10 15

10
Ser Tyr Gly Ala Ala Trp Leu Leu Leu Xaa Pro Ala Gly Ser Ser Arg
20 25 30

Val Glu Pro Thr Gln Asp Ile Ser Ile Ser Asp Gln Leu Gly Gly Gln
35 40 45

15
Asp Val Pro Val Phe Arg Asn Leu Ser Leu Leu Val Val Gly Val Gly
50 55 60

Ala Val Phe Ser Leu Leu Phe His Leu Gly Thr Arg Glu Arg Arg Arg
65 70 75 80

20
Pro His Ala Xaa Glu Pro Gly Glu His Thr Pro Leu Leu Ala Pro Ala
85 90 95

Thr Ala Gln Pro Leu Leu Leu Trp Lys His Trp Leu Arg Glu Xaa Ala
100 105 110

25
Phe Tyr Gln Val Gly Ile Leu Tyr Met Thr Thr Arg Leu Ile Val Asn
115 120 125

30
Leu Ser Gln Thr Tyr Met Ala Met Tyr Leu Thr Tyr Ser Leu His Leu
130 135 140

Pro Lys Lys Phe Ile Ala Thr Ile Pro Leu Val Met Tyr Leu Ser Gly
145 150 155 160

35
Phe Leu Ser Ser Phe Leu Met Lys Pro Ile Asn Lys Cys Ile Gly Arg
165 170 175

40
Asn

(2) INFORMATION FOR SEQ ID NO: 322:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

50
Arg Ile Thr Asp Asn Pro Glu Gly Lys Trp Leu Gly Arg Thr Ala Arg
1 5 10 15

55
Gly Ser Tyr Gly Tyr Ile Lys Thr Thr Ala Val Glu Ile Xaa Tyr Asp
20 25 30

Ser Leu Lys Leu Lys Lys Asp Ser Leu Gly Ala Pro Ser Arg Pro Ile
35 40 45

60
Glu Asp Asp Gln Glu Val Tyr Asp Asp Val Ala Glu Gln Asp Asp Ile

368

50 55 60

Ser Ser His Ser Gln Ser Gly Ser Gly Gly Ile Phe Pro Pro Pro Pro
65 70 75 80

5 Asp Asp Asp Ile Tyr Asp Gly Ile Glu Glu Glu Asp Ala Asp Asp Gly
 85 90 95

10 Phe Pro Ala Pro Pro Lys Gln Leu Asp Met Gly Asp Glu Val Tyr Asp
 100 105 110

Asp Val Asp Thr Ser Asp Phe Pro Val Ser Ser Ala Glu Met Ser Gln
 115 120 125

15 Gly Thr Asn Val Gly Lys Ala Lys Thr Glu Glu Lys Asp Leu Lys Lys
 130 135 140

Leu Lys Lys Gln Xaa Lys Glu Xaa Lys Asp Phe Arg Lys Lys Phe Lys
20 145 150 155 160

Tyr Asp Gly Glu Ile Arg Val Leu Tyr Ser Thr Lys Val Thr Thr Ser
 165 170 175

25 Ile Thr Ser Lys Lys Trp Gly Thr Arg Asp Leu Gln Val Lys Pro Gly
 180 185 190

Glu Ser Leu Glu Val Ile Gln Thr Thr Asp Asp Thr Lys Val Leu Cys
 195 200 205

30 Arg Asn Glu Glu Gly Lys Tyr Gly Tyr Val Leu Arg Ser Tyr Leu Ala
 210 215 220

Asp Asn Asp Gly Glu Ile Tyr Asp Asp Ile Ala Asp Gly Cys Ile Tyr
35 225 230 235 240

Asp Asn Asp

40 (2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

50 Ser Met Ser Ala Leu Thr Arg Leu Ala Ser Phe Ala Arg Val Gly Gly
1 5 10 15

Arg Leu Phe Arg Ser Gly Cys Ala Arg Thr Ala Gly Asp Gly Gly Val
 20 25 30

55 Arg His Ala Gly Gly Gly Val His Ile Glu Pro Arg Tyr Arg Gln Phe
 35 40 45

Pro Gln Leu Thr Arg Ser Gln Val Phe Gln Ser Glu Phe Phe Ser Gly
 50 55 60

60 Leu Met Trp Phe Trp Ile Leu Trp Arg Phe Trp His Asp Ser Glu Glu

369

65

70

75

80

Val Leu Gly His Phe Pro Tyr Pro Asp Pro Ser Gln Trp Thr Asp Glu
85 90 95

5

Glu Leu Gly Ile Pro Pro Asp Asp Glu Asp
100 105

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 73 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 7, 1997	Accession Number 97923
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>73</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 22, 1997	Accession Number 209071
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 73 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit February 25, 1998	Accession Number 209641
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 75 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit July 24, 1997	Accession Number 209179
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>77</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 7, 1997	Accession Number 97924
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g.: "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 80 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 13, 1997	Accession Number 97958
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	2004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 80 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 22, 1997	Accession Number 209072
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>80</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit September 4, 1997	Accession Number 209235
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 84 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit August 28, 1997	Accession Number 209226
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 84, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 13, 1997	Accession Number 97957
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>84</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>May 22, 1997</u>	Accession Number <u>209073</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

5 (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

10 (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

15 (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

20 (f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

25 (i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

30 3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.
- 5
5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
- 10
6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
- 15
7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.
8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.
- 20
9. A recombinant host cell produced by the method of claim 8.
10. The recombinant host cell of claim 9 comprising vector sequences.
11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:
- 25
- (a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;
- 30
- (c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- 35
- (e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

5 12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

10 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15 15. A method of making an isolated polypeptide comprising:

- (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
- (b) recovering said polypeptide.

20 16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

25 18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

30 (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

35 (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:
- 5 (a) contacting the polypeptide of claim 11 with a binding partner; and
(b) determining whether the binding partner effects an activity of the polypeptide.
21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.
- 10 22. A method of identifying an activity in a biological assay, wherein the method comprises:
- (a) expressing SEQ ID NO:X in a cell;
(b) isolating the supernatant;
(c) detecting an activity in a biological assay; and
15 (d) identifying the protein in the supernatant having the activity.
23. The product produced by the method of claim 22.